

FIGURE 1A

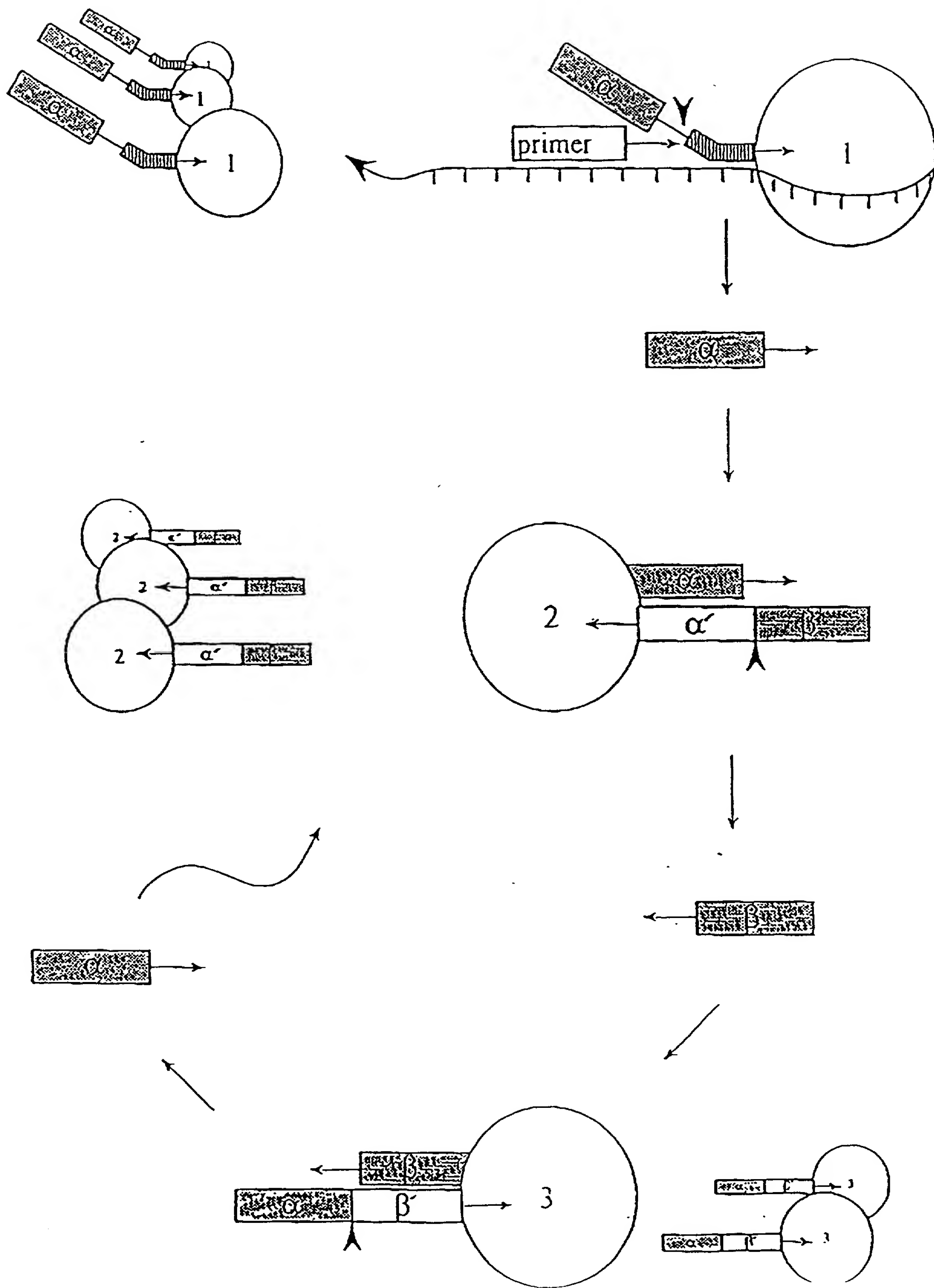
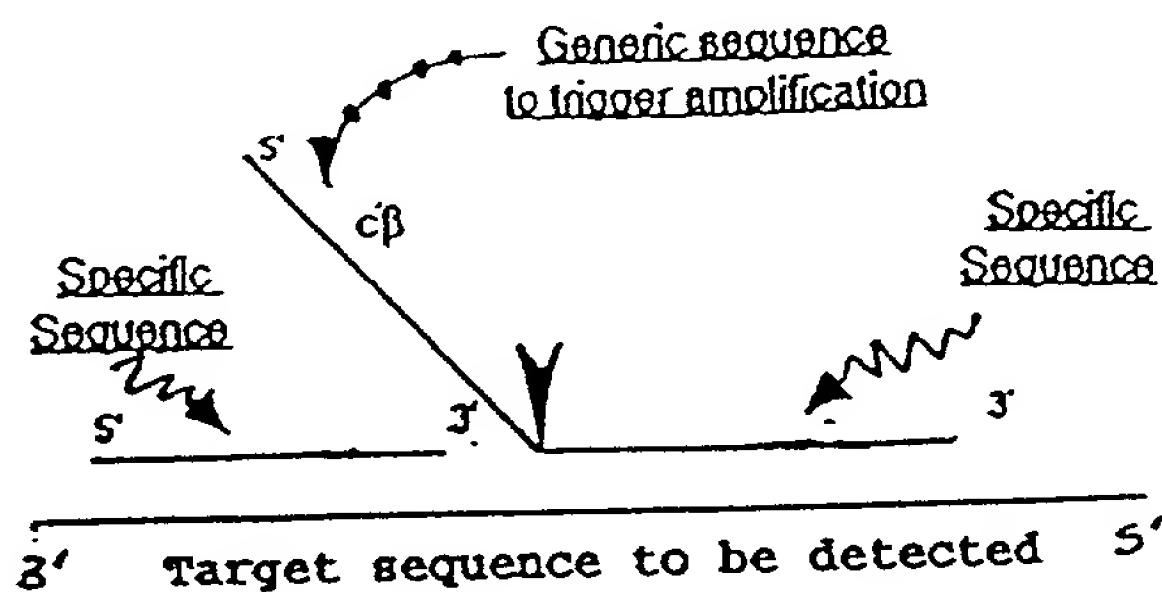
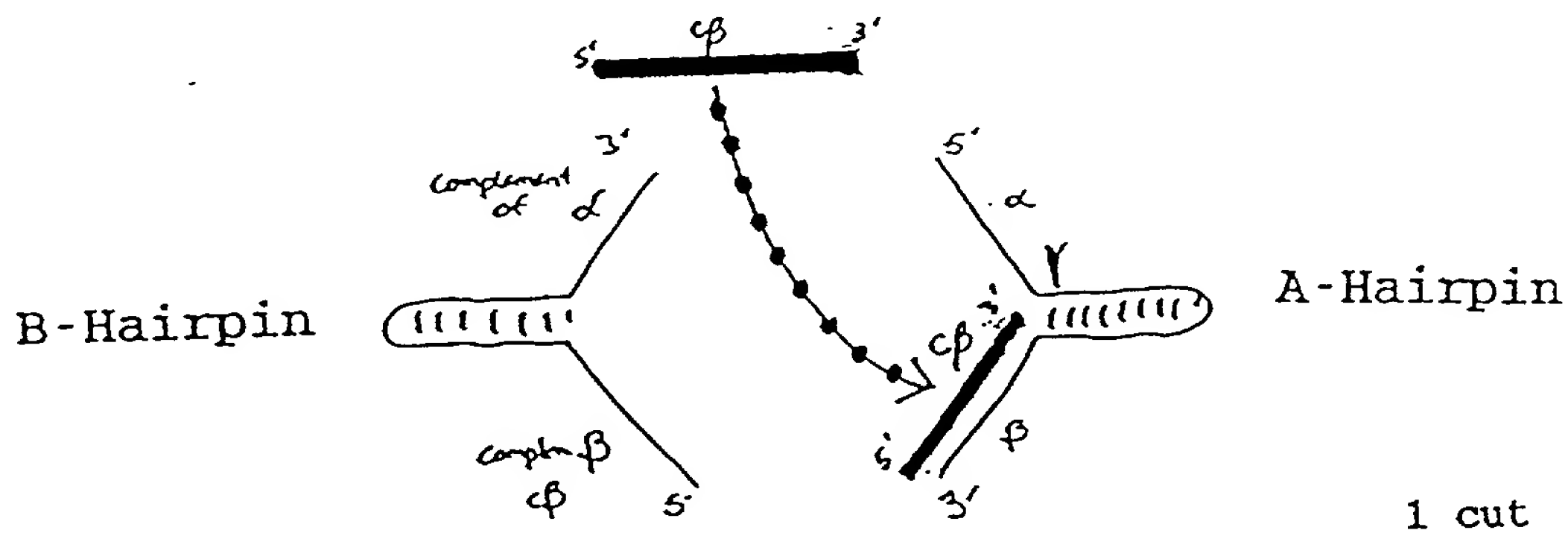


FIGURE 1 B

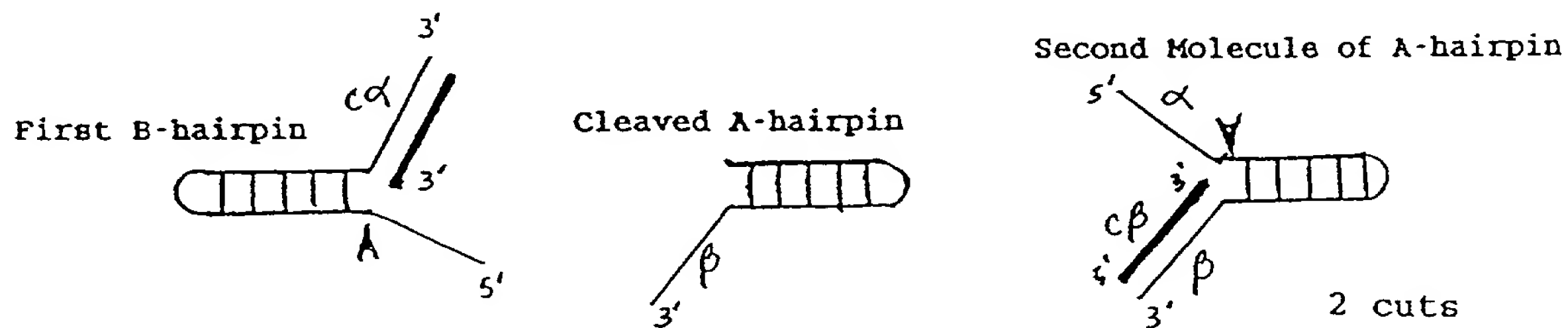
PART ONE: TRIGGER REACTION



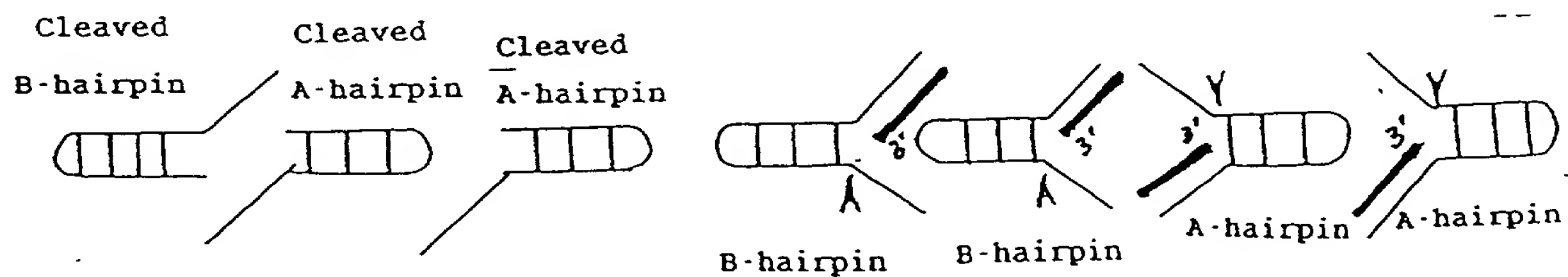
PART TWO: DETECTION REACTION



Denature, anneal



Denature, anneal



4 cuts

FIGURE 2 (cont'd)

AJORITY (SEQ ID NO:7)	CGAGCGGGACGACGTXCTGGCCACCCCTGGCCAAAGAGGGGGAAGGAGGGGTACGAGGTGGGGATCCTC	417
NAPTAQ (SEQ ID NO:1)G.....G.....C.....C.....	414
NAPTFL (SEQ ID NO:2)	T.....G.....CG.....	420
NAPTTH (SEQ ID NO:3)T..C.....	
AJORITY	ACCGCGGACCGGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGCTCCTCCACCGCGAGGGGTACCTCA	487
NAPTAQAAA.....T.....CA.....	484
NAPTFL	..T.....G.....G.....A.....T.....G.....	490
NAPTTHA..G.C.....G.....CC.....	
AJORITY	TCACCCCGCGGTGGCTTTGGGAGAAGTACGGGCTGAGGCGCGGAGCAGTGGGTGGACTACCGGGCGCTGGC	557
NAPTAQC.....A.....A.....C..G.....CC.....A.	554
NAPTFLAC.....C.....C.....T...C.....C..T	560
NAPTTHA.....C.....	
AJORITY	CGGGGACCCCTCCGACAACTCCCGGGGTCAAGGGCATCGGGGAGAGAGCCGCCXGAAGCTCCTCXAG	627
NAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	624
NAPTFLG..T...A.....G.....A..G.....A..CGC	630
NAPTTH	
AJORITY	GAGTCGGGGAGCCCTGGAAACCTCCTCAAGAACCTCGACCGGGTGAAGCCCGG...CXTCCGGGAGAGA	694
NAPTAQGC.....C.....A.....	691
NAPTFLT..C..C.....A.....T...T.G.....C	700
NAPTTHA.....A.....A.AAAA.G.....	

6

6

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCCGCCGCCCTCGAGGAGGAGCTCTCCGCCCTGGCCGCCACCCGTTCAACCTCAACTCCCGGGAC	1464
DNAPTAO (SEQ ID NO:1)GC.....CC.....	1461
DNAPTFL (SEQ ID NO:2)	...G.G...AG..G.....T.....G.....	1470
DNAPTTH (SEQ ID NO:3)	
MAJORITY	CAGCTGGAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGACXGGCAAGC	1534
DNAPTAOC.....A.....	1531
DNAPTFLGC.....G..G..G..T.....G..G..A..	1540
DNAPTTHTA.....T.G..G.....C.A.....A.....	
MAJORITY	GCTCCACGAGCGCGCGCTGCTGGAGCGGCTXCGXGAGGGCCACCGCATCGTGGAGAGATCCTGCCAGTA	1604
DNAPTAOC.....C..C.....	1601
DNAPTFLT.....G..A.....CGGC.....C...C..	1610
DNAPTTHG.....A..G.....	
MAJORITY	CGGGGAGCTCACCAAGCTCAAGAACAGCTACATXGACCGCGCTGCCXGXCCTCGTCCACCGCCAGGACGGGGC	1674
DNAPTAOG...G.....T.....G.A...A.....	1671
DNAPTFLA.....A.....G..G.....A...C...	1680
DNAPTTHG.G.....C..AAG.....G.....	
MAJORITY	CGCCTCCACACCGGCTTCAACCAGACGGGCCACGGCCACGGGCGAGGCTTAGTAGCTCCGAGCCCAACCTGC	1744
DNAPTAOA.....T.....C..	1741
DNAPTFLG.....C.....TCC.....	1750
DNAPTTHG.....	

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCGCAAGGTGCGGGCGCTGGATTGAGAAAGACCCCTGGAGAGGGCAGGCGGGGTACGTGGAGA	2164
DNAPTAA (SEQ ID NO:1)	2161
DNAPTFL (SEQ ID NO:2)G.....G.....T.....	2170
DNAPTTH (SEQ ID NO:3)A.....G.....A.....A.....	
MAJORITY	CCCTCTTCGGCGCGCGCGCTAGGTGCCCGACCTCAACGCCCGGCTGAAGAGCGTGGCGGAGCGCGCGGA	
DNAPTAAC.....A.....AG.G.....C..	2234
DNAPTFLT.....	2231
DNAPTTHAA.AA.....CA.....C.....	2240
MAJORITY	GGGCATGGCCCTTCAACATGCCCGTCCAGGGCACCGCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAAG.....T.....	2304
DNAPTFLG.....	2301
DNAPTTHG.....	2310
MAJORITY	TTCCCGCGGCTXCAGGAATGGGGCGCAGGATGCTCCTXCAGGTCCACGAGAGCTGGTCCGAGGCGCC	
DNAPTAAA.....GG.....T.....	2374
DNAPTFLT.....G.....TT.G.....G.....	2371
DNAPTTHC.....G.....C.....G.....	2380
MAJORITY	CCAAAGAGCGCGCGGAGGXGCTGGCGCGCTTGGCCAGGAGGTGATGGAGGGGCTCTATCCCGCTGGCGCT	
DNAPTAAA.....CG.....CGG.....G.....	2444
DNAPTFLG.....AG.....A.....AA..C.....CAG..	2441
DNAPTTHC.....C.....A.....G.....C.....C.....	2450

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGCCCTGGAGGTGGAGGTGGGGATGGGGAGGACTGGCTCTCCGCCAAGGAGTAG	2499
DNAPTAA	(SEQ ID NO:1)A.....GA	2496
DNAPTLL	(SEQ ID NO:2)CC.....GT...	2505
DNAPTHH	(SEQ ID NO:3)T.....GT...	

FIGURE 3

MAJORITY (SEQ ID NO:8)	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLLKALKEDG·DAVXVVVFDKAK	
TAQ PRO (SEQ ID NO:4)	RG.....H.....	69
TRL PRO (SEQ ID NO:5)V.....	68
TTH PRO (SEQ ID NO:6)YK..F.....	70
MAJORITY	APSRHEAYEAYKAGRPTPEDFPRQLALIKELVDLGLXRLEVPGEADDVLATLAKKAKEGVEVRIL	
TAQ PRO	GG.....A.....S.....	139
TRL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPNSDNLPGVKGI GEKTAXKLLX	
TAQ PRO	K.....H.....D..A.....T..E.....R...E	209
TRL PROE...I.....Y.....A.....I.....QR..I	208
TTH PROV...V.....H...E.....F...V.....L...K	210
MAJORITY	EWGSLNLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRFLERLEF	
TAQ PRO	A.....L...·A...L...D...K...WD.AK.....K.....R.....	278
TRL PRO	FQH...Q...·SL...LQ.G...A.A...RK...Q.H.....GR..T.NL.....	277
TTH PROENV...K...L...R...LE..R.....L.QG.....	280
MAJORITY	GSLLHEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMYAEELLALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PRO	S.....K.....D.....G.....PE.YKA.....A	348
TRL PRO	G...A.....L...SF.....G.WE..L...Q...R.....G.	347
TTH PROA.AP.....K...C.D.....A...A...K.....	350

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FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKDLAVLALREGLDLXPGDDPML LAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)S.....G.P.....E.....A.....A.....WG	418
TR PRO (SEQ ID NO:5)I.....F.E.....A.....QT..KE	417
TTH PRO (SEQ ID NO:6)S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWL YXEVEKPLSRVL AHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PROR...R...A.....R.....A.....A.....	488
TR PROK.....E.....R.....EA.V.Q.....	487
TTH PROK.....H.....L.....	490
MAJORITY	QLERVLFDLGLPAIGKTEKTGRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLXPXLVHPRTG	
TAQ PROS.....S.....D.I.....	558
TR PRODR.....A.....K..	557
TTH PROR...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNQTATATGRLSSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PROI.....L.....	628
TR PROV..V.....	627
TTH PROA..A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPPEAVDPLMRRAAKTI NFGVLYGMSAHRLSQELAI PYEEAVAFIERYFQ	
TAQ PROE.....R.....Q.....	698
TR PROS..G.....G..S.....	697
TTH PROK.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRWIEKTL EGRRRGYVETLFGRRRYVPDLNARVKSUREAERMAFNMPVQGTADLMKLAHVKL	768
TAQ PR0 (SEQ ID NO:4)E.....	767
TRL PR0 (SEQ ID NO:5)	Y.....G.....	770
TTH PR0 (SEQ ID NO:6)K.....	
MAJORITY	FPR LXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PR0E.....	833
TRL PR0Q.L.....	831
TTH PR0R.....	835
L.....QA.....E.....A...KA.....M.....G	
E.....A...R.....W...d.....L.....	
D.....R.....	

FIGURE 4

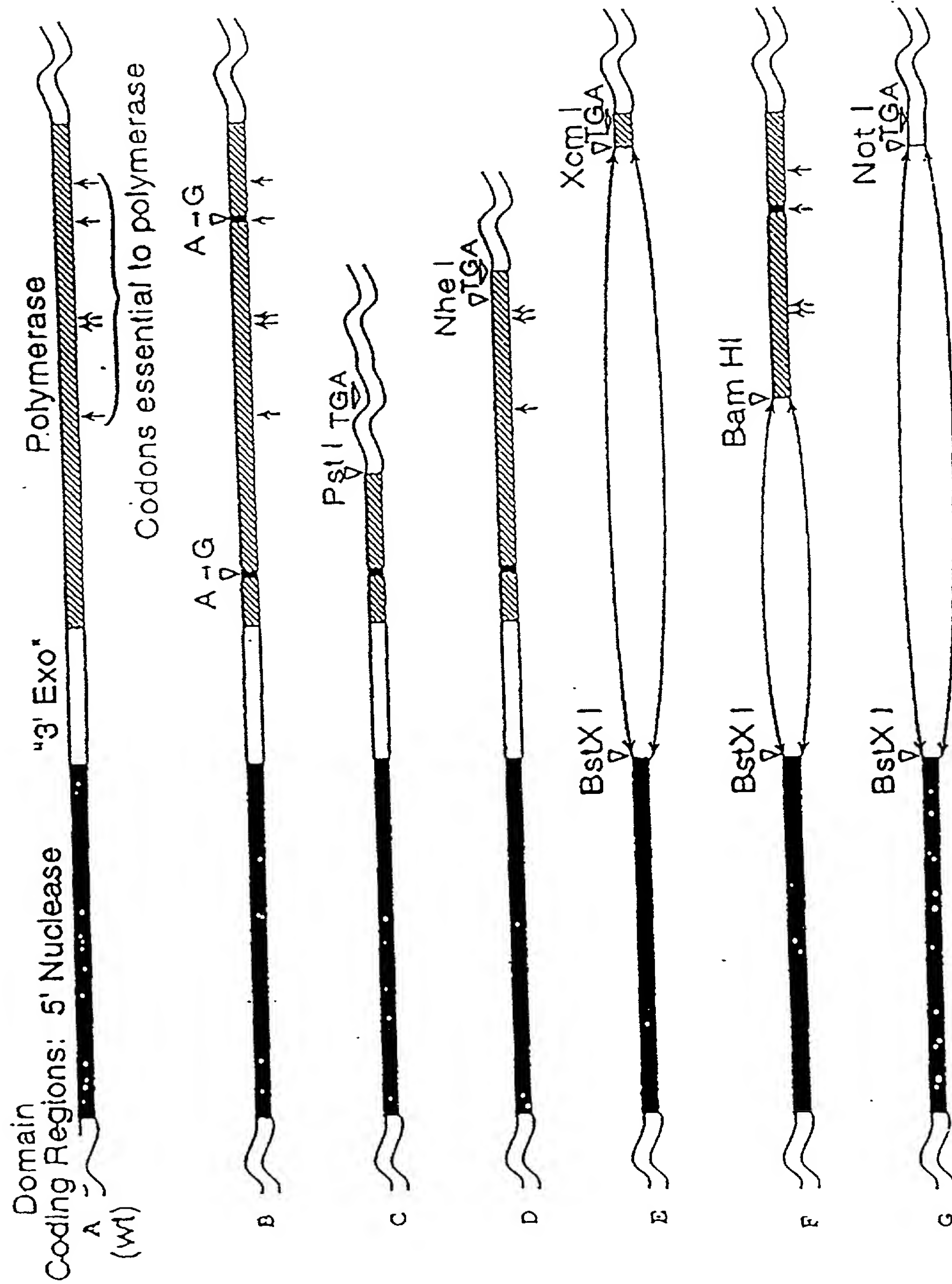
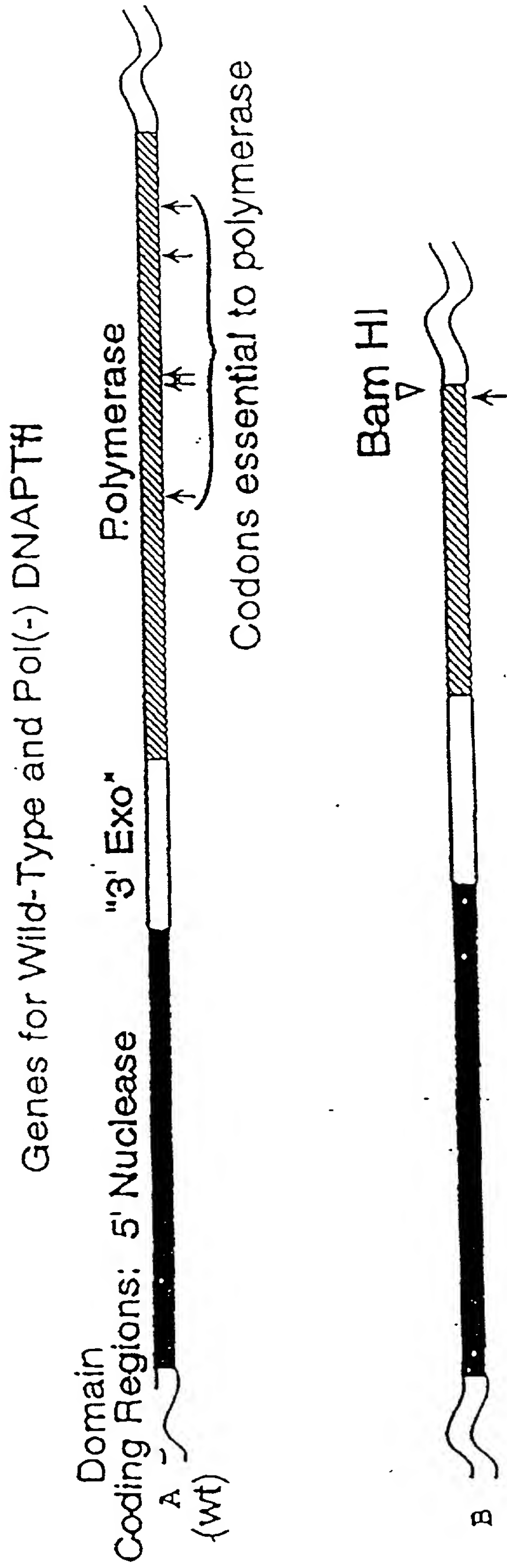


FIGURE 5



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FIGURE 6

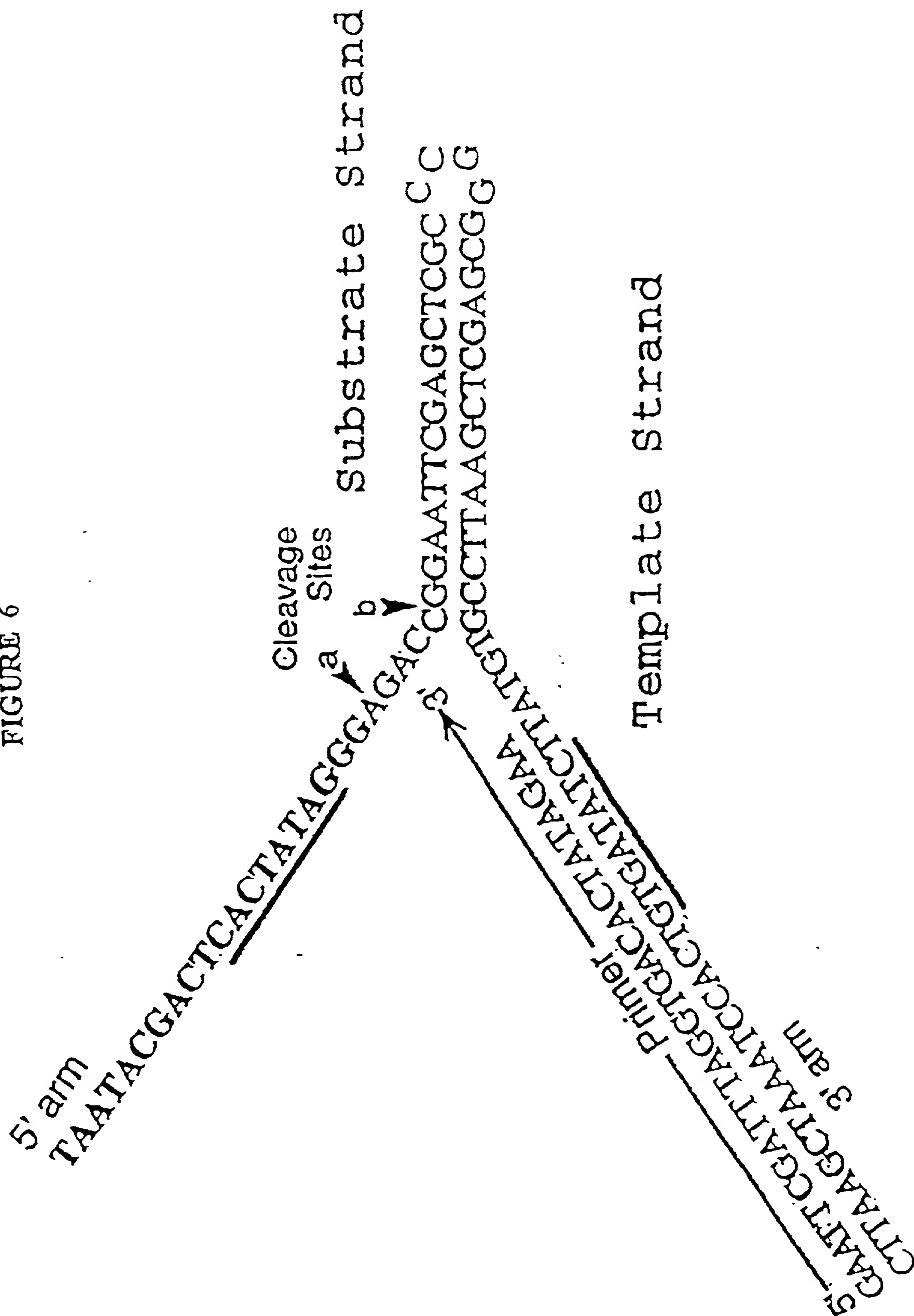


FIGURE 7



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FIGURE 8

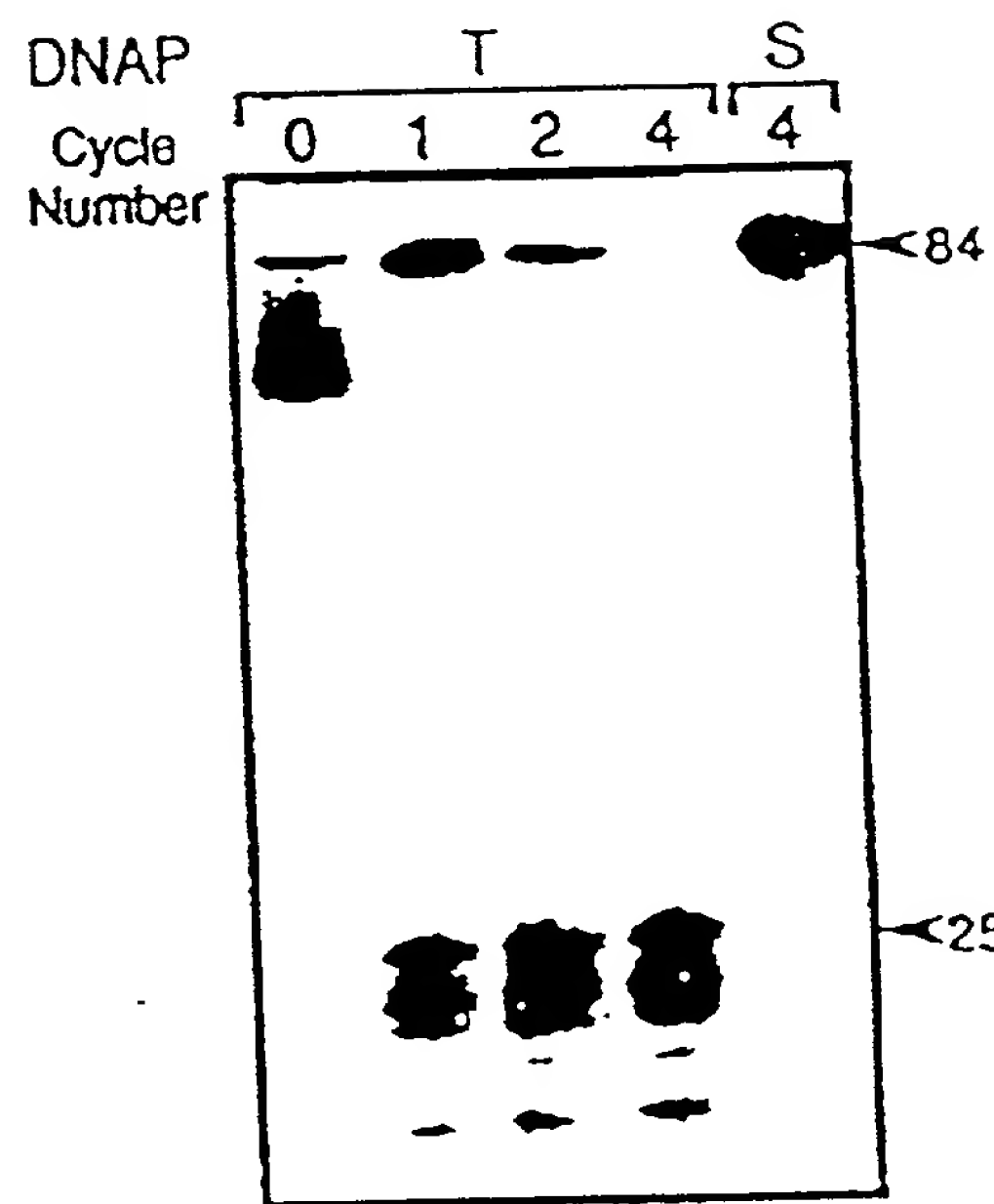
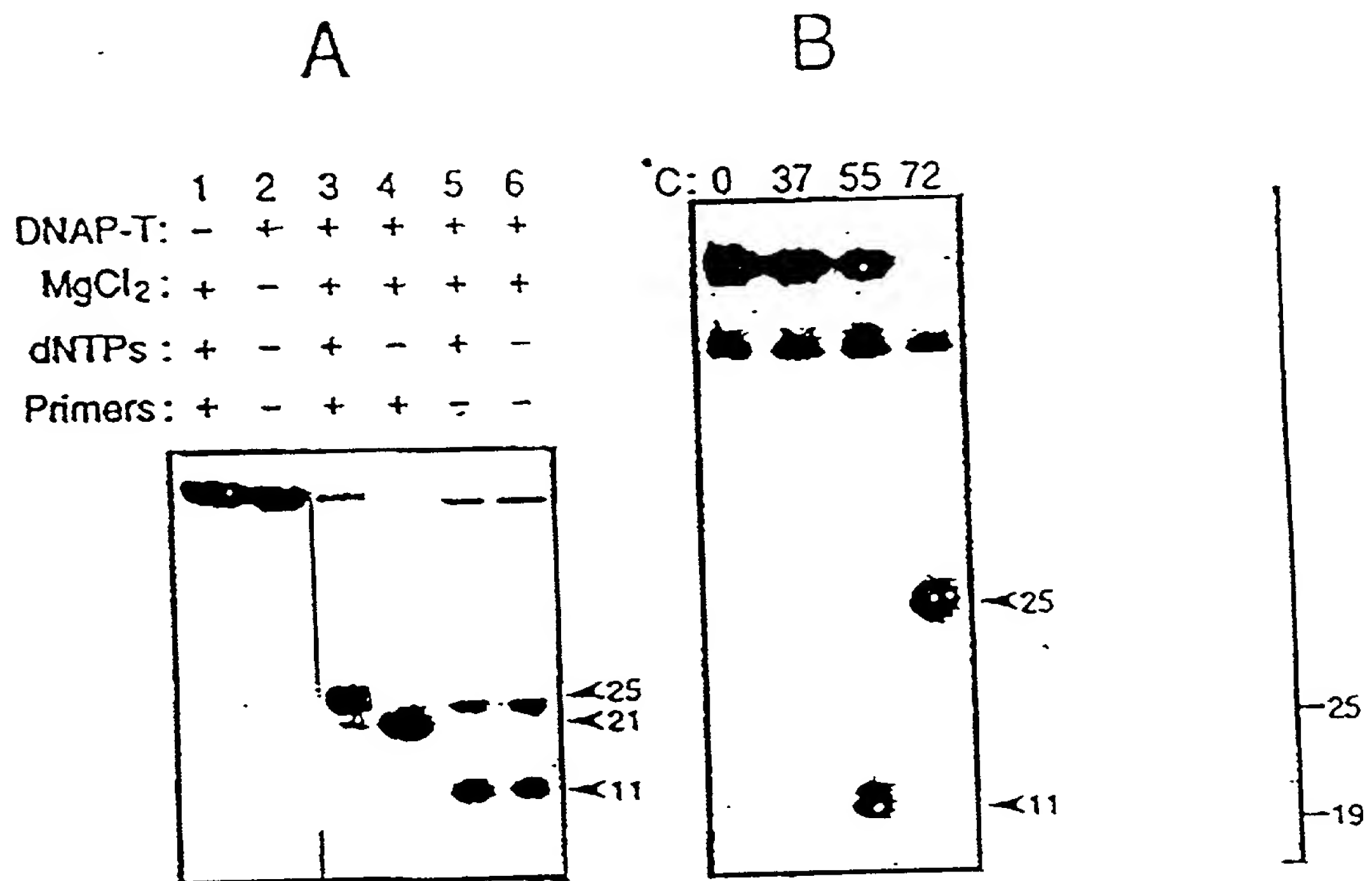
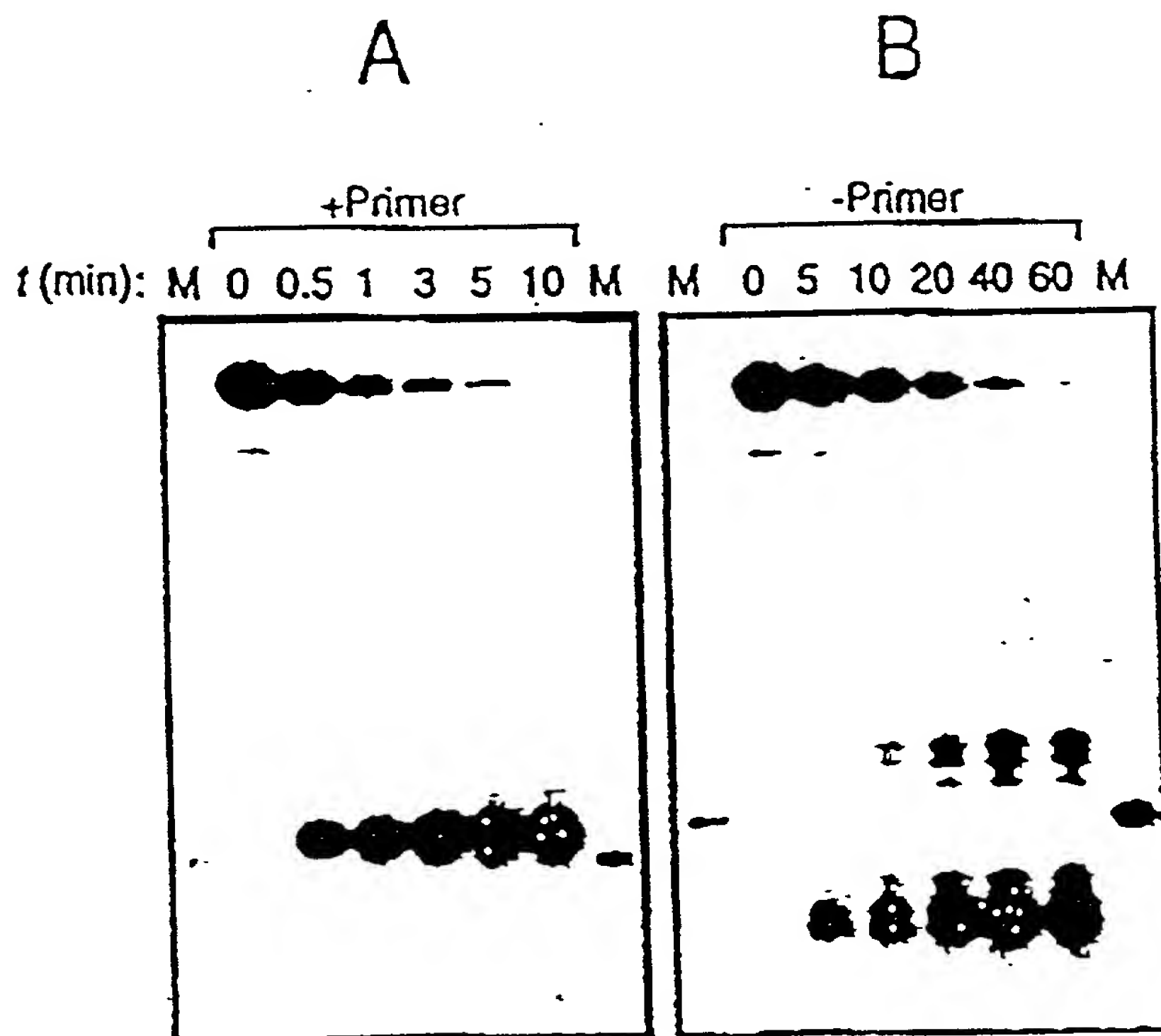


FIGURE 9



094093-02301
03230 0360450

FIGURE 10



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FIGURE 11

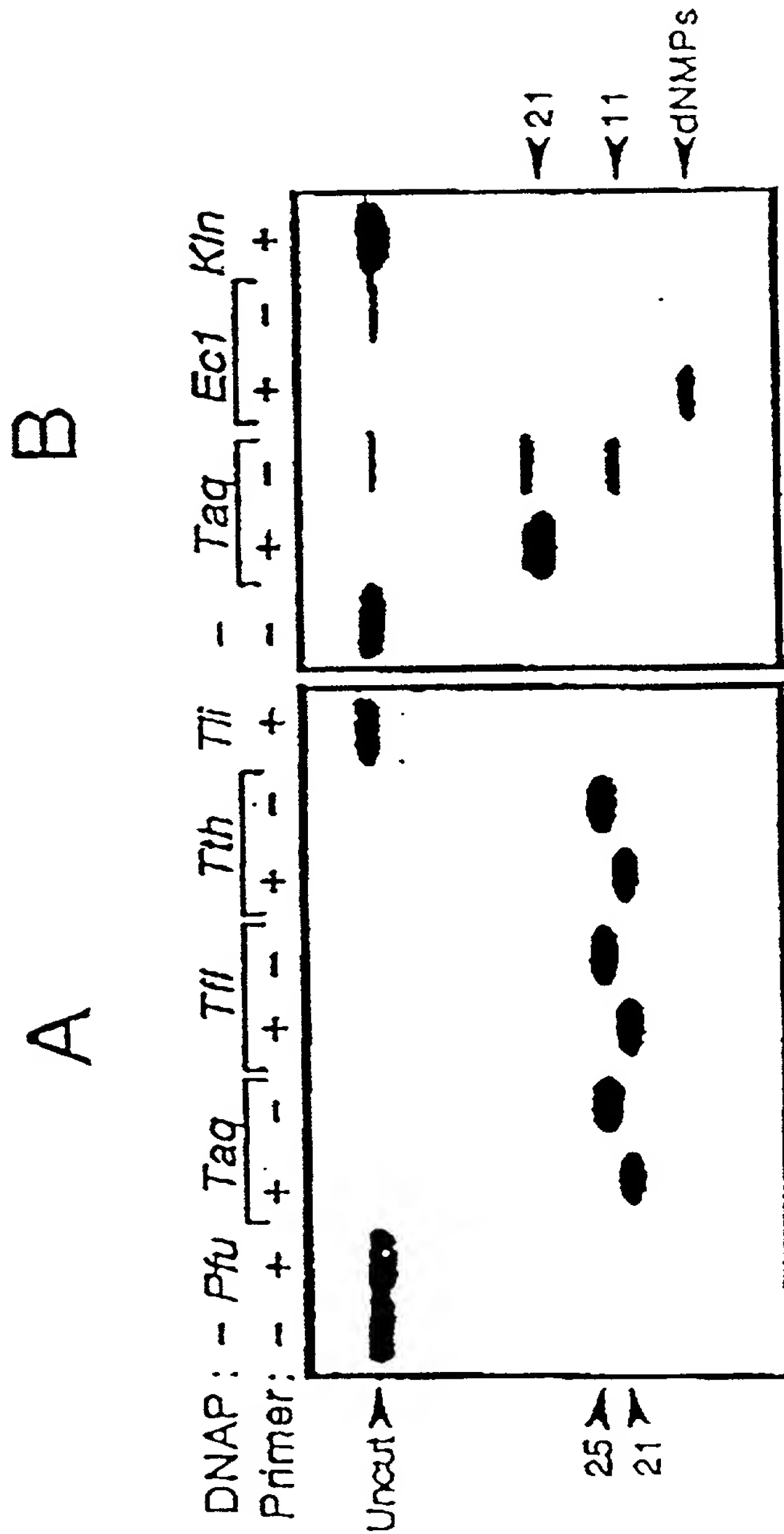


FIGURE 12

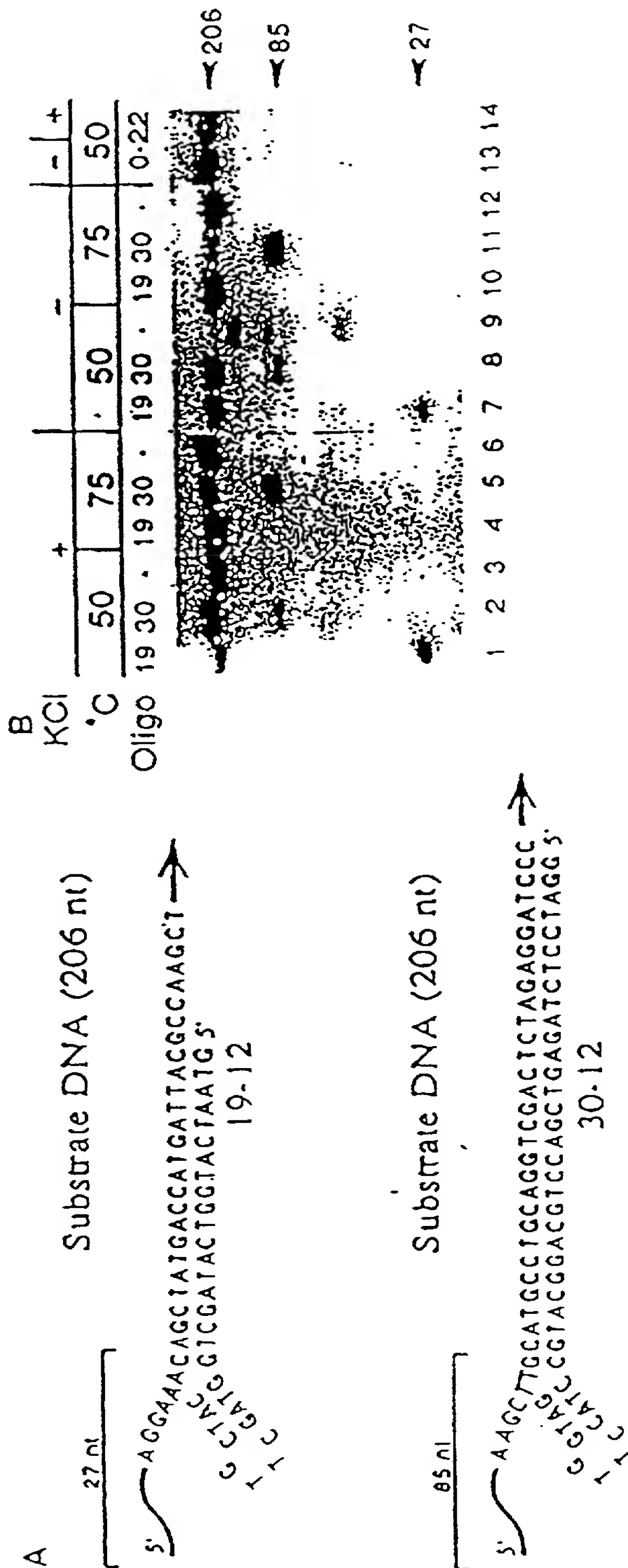


FIGURE 13

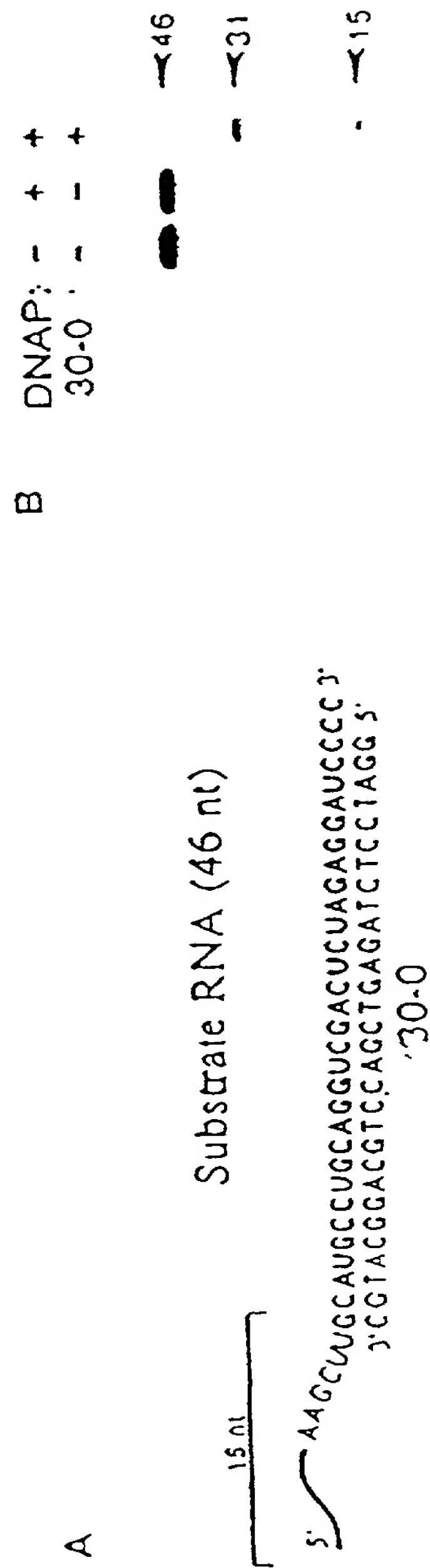


FIGURE 14

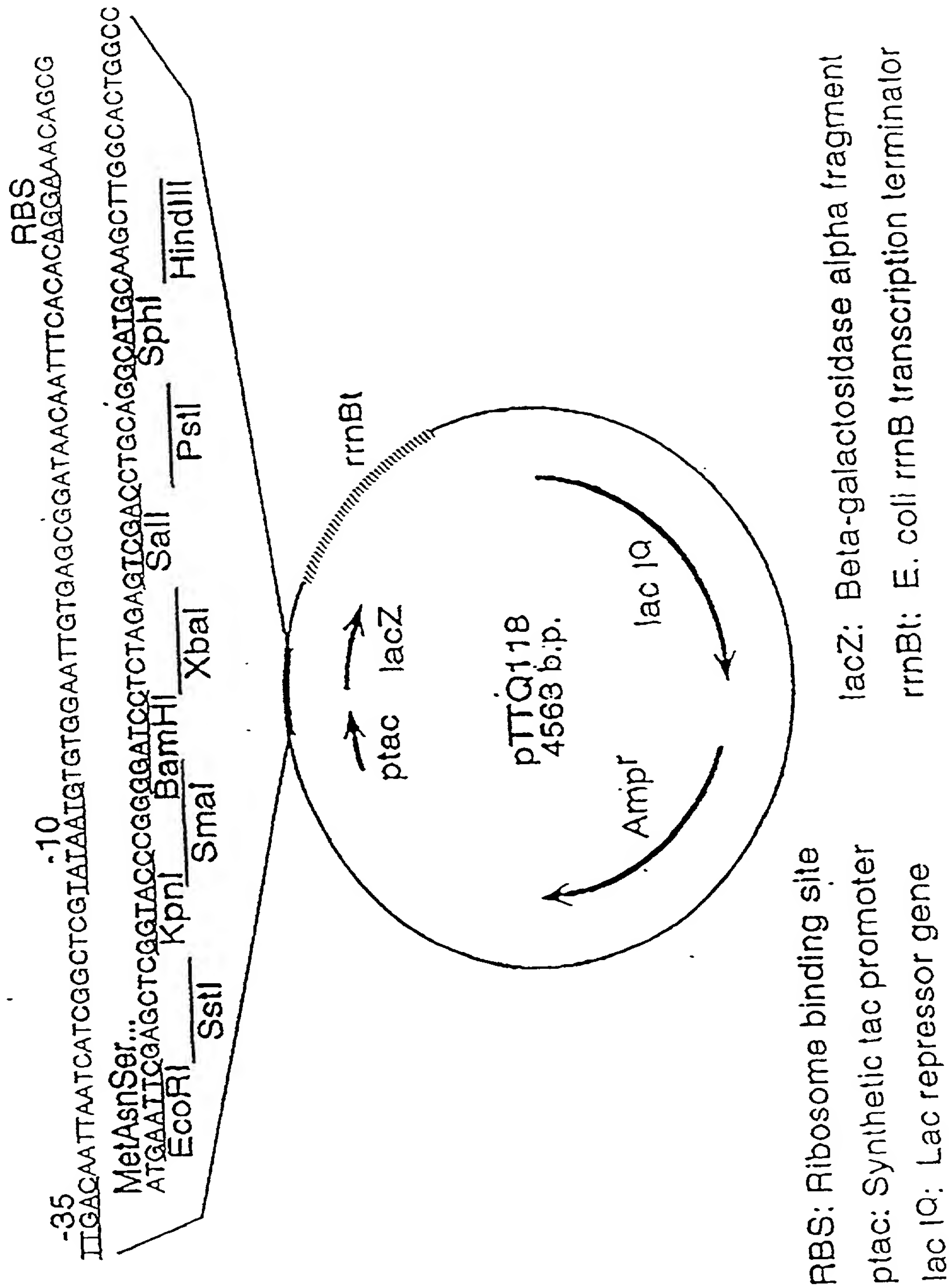
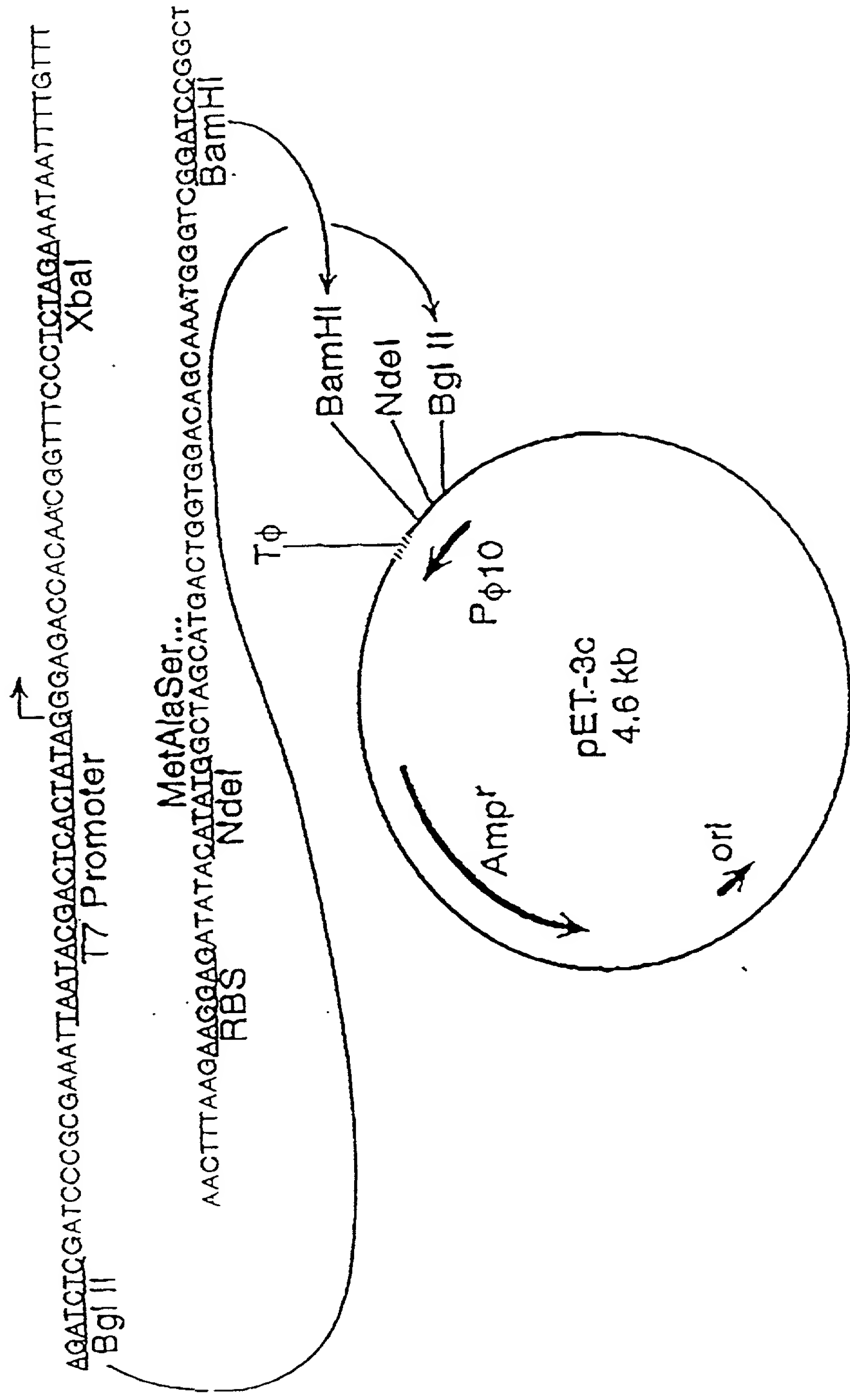


FIGURE 15



RBS: Ribosome binding site

Pφ10: Bacteriophage T7 φ10 promoter

Tφ: T7 φ Terminator

FIGURE 16

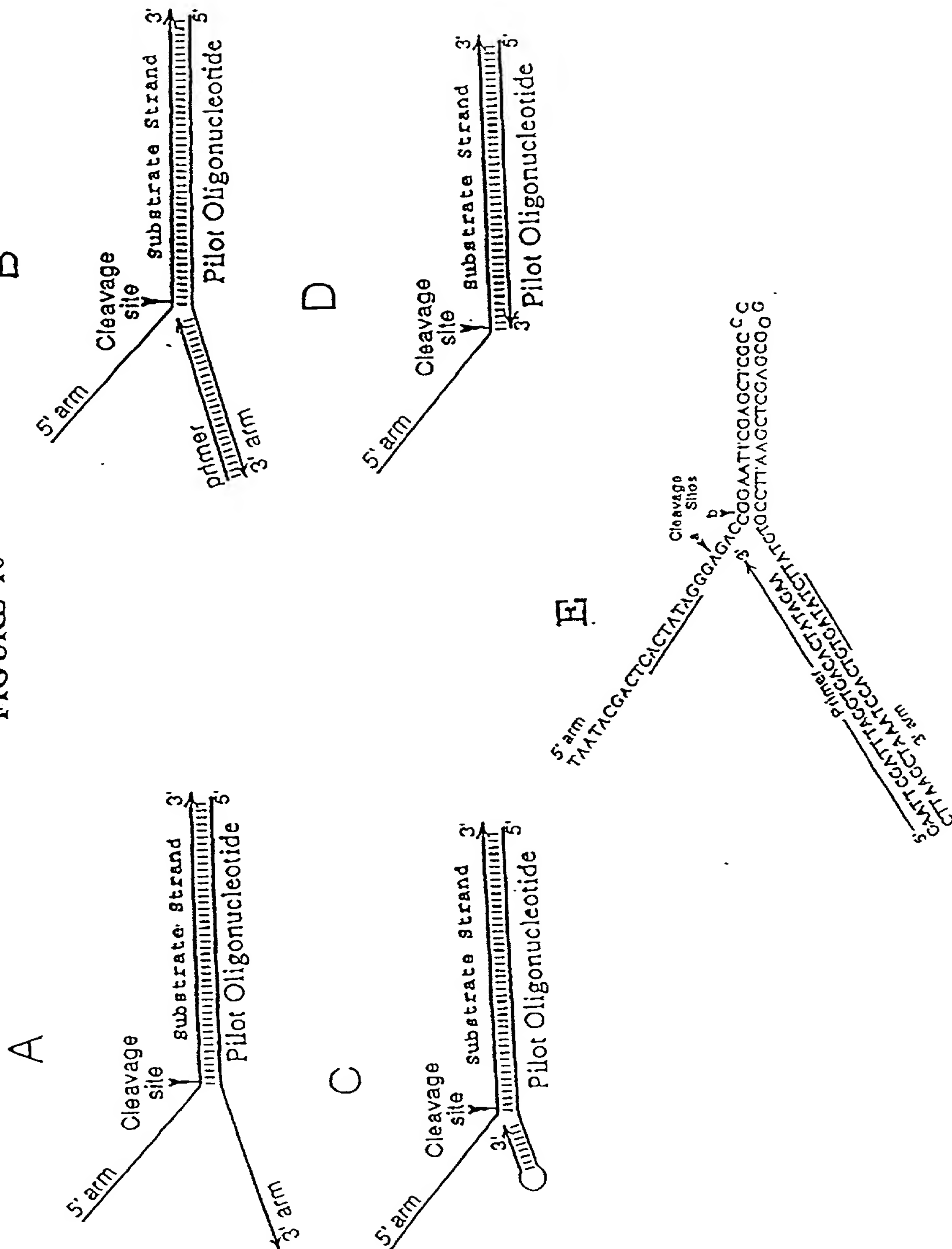


FIGURE 17

1 2 3 4 5 6 7

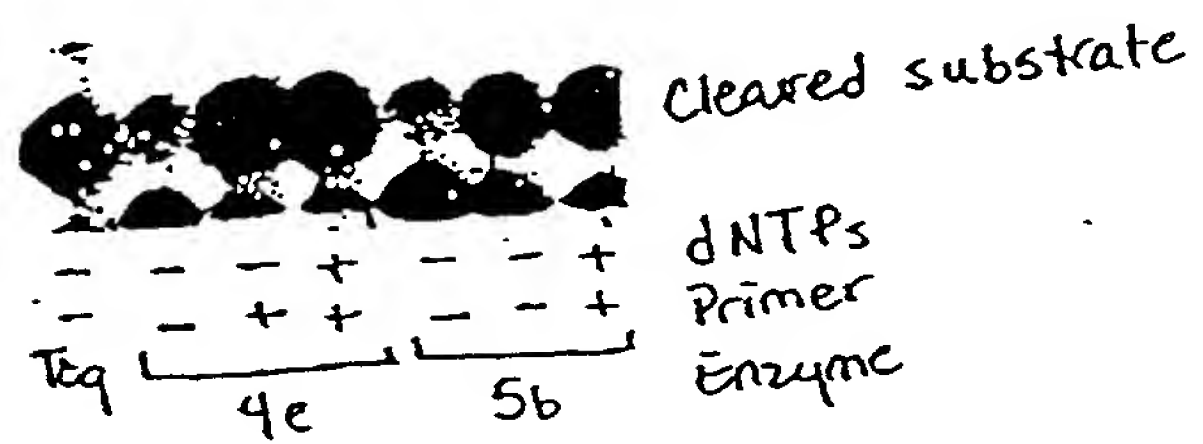
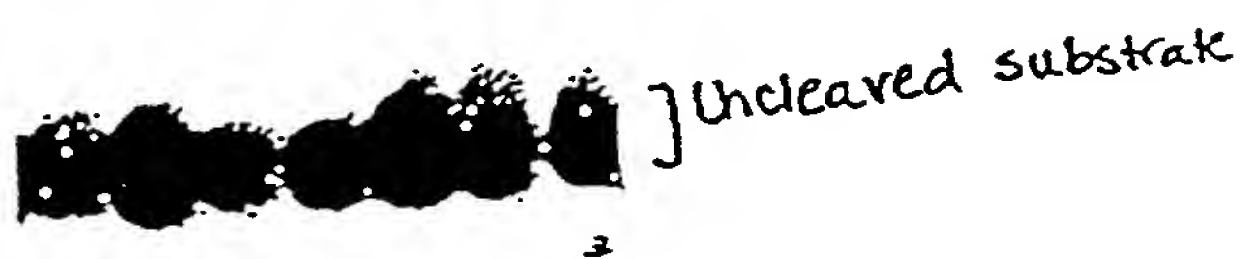


FIGURE 18

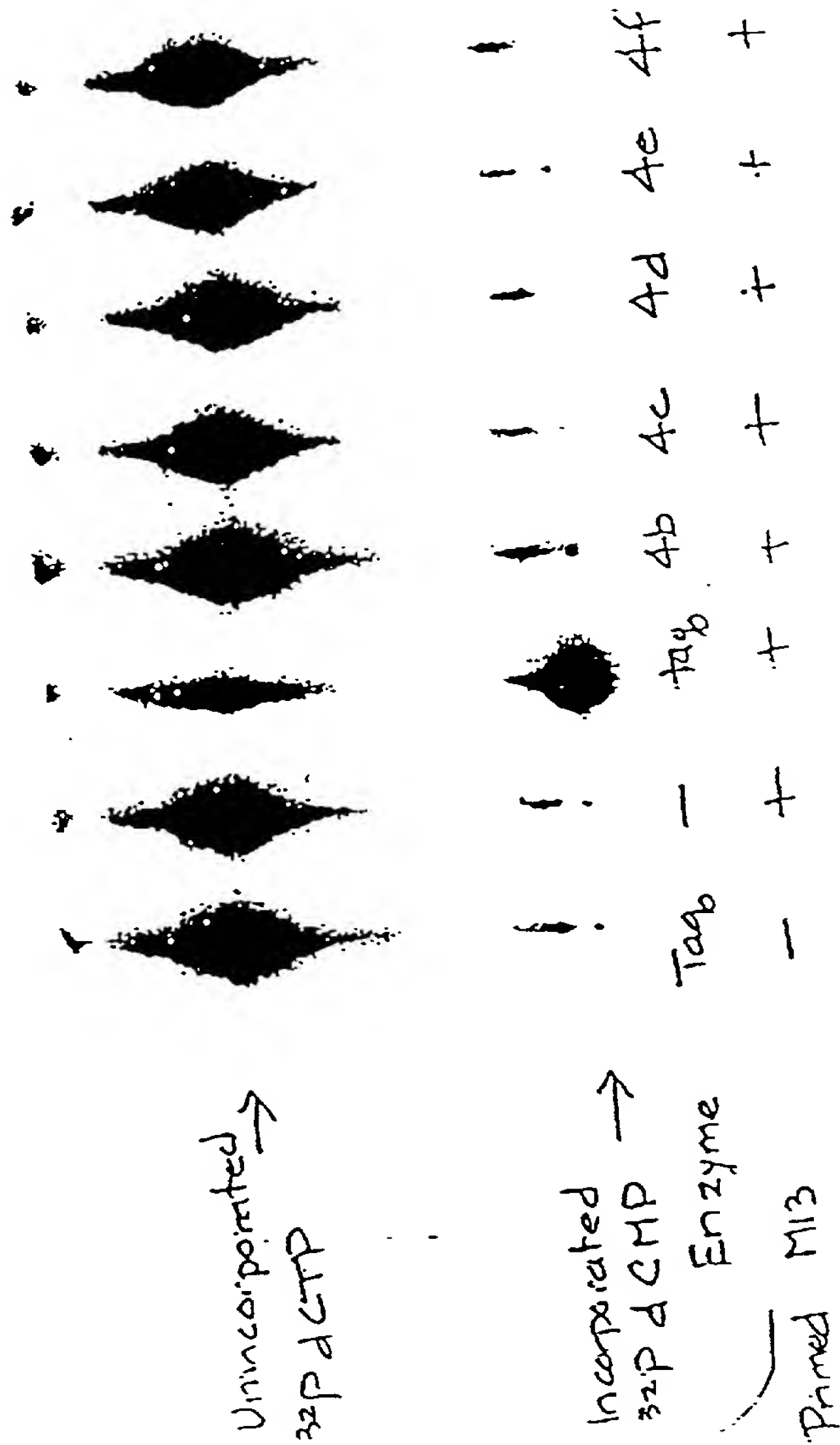
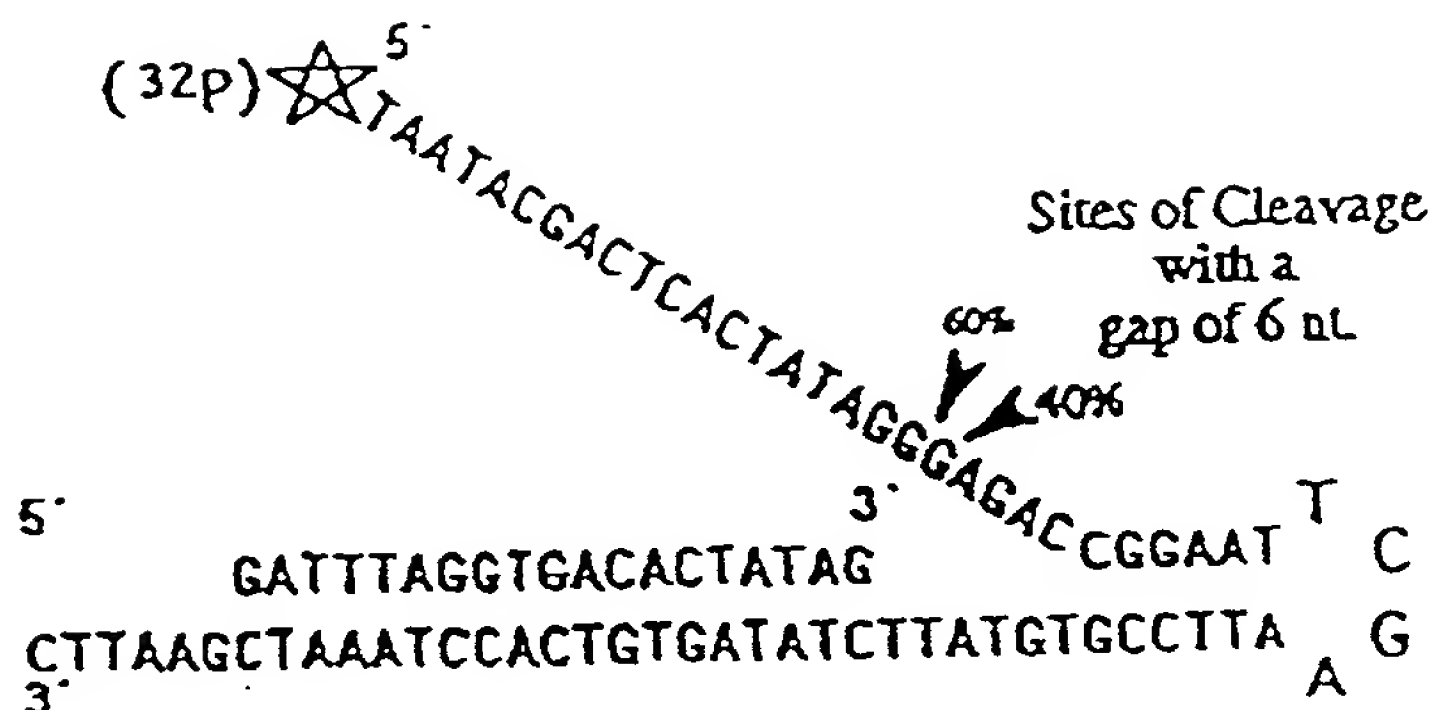




FIGURE 19

A



B

4d		4b		(2 pt. mutation)		Unmodified	
Rel. activity		small activity		DNM Tag			
1	2	3	4	5	6	7	8
C +		T +		T +		ATP	

84 nt →  ← harpin test molecule
 →  ← conversion to double stranded (complete extension of primer)

desired product 21 nt.

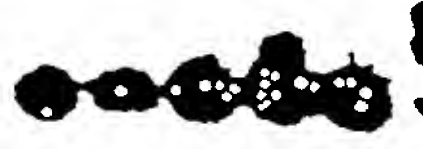
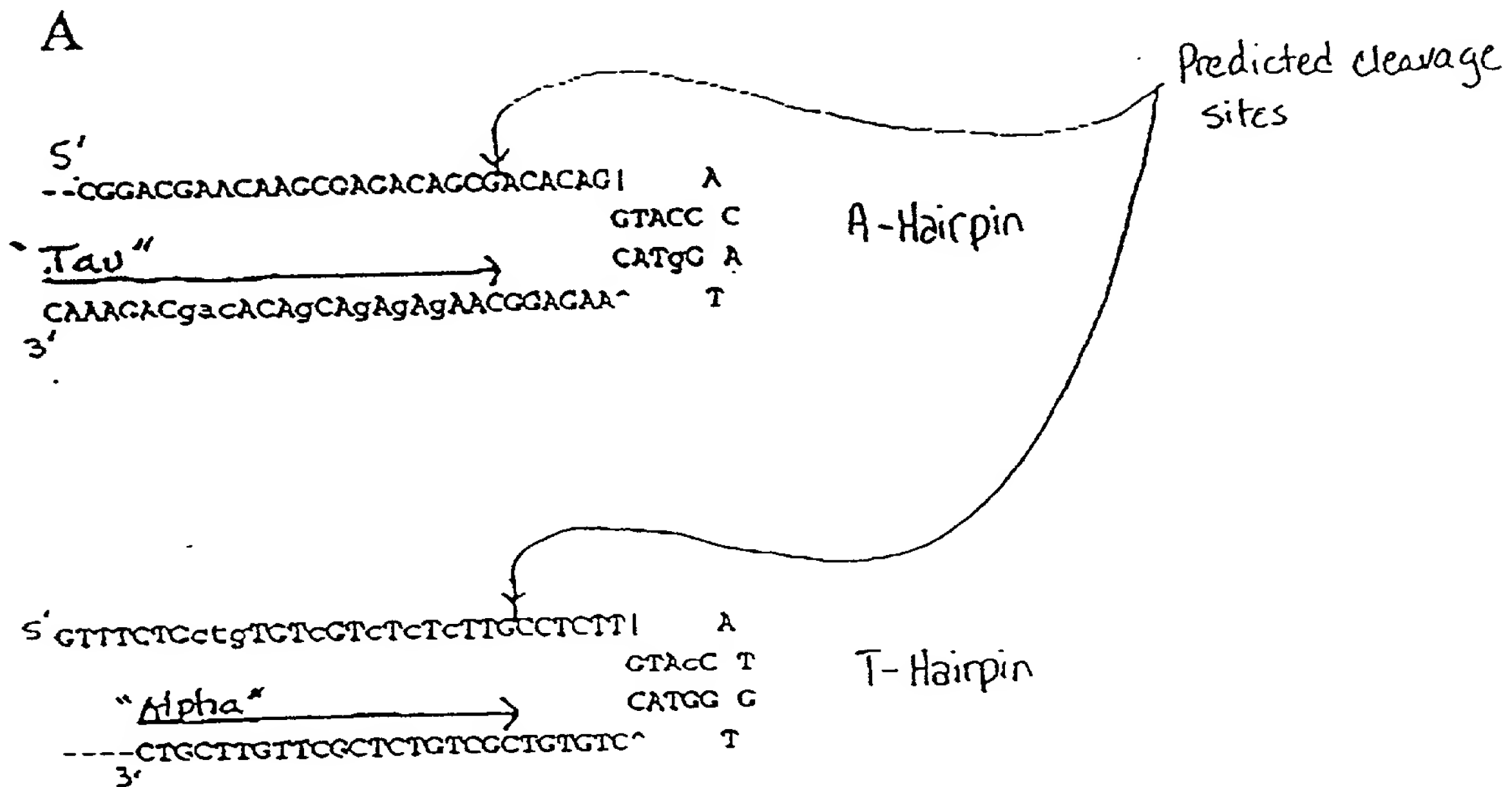
→  } Multiple bands caused by polymerization
 ↑ some aberrant cleavage with "4b" because of residual polymerase activity.

FIGURE 20



B Sequence of alpha primer:

5' GAC GAA CAA CCG AGA CAG CG 3'

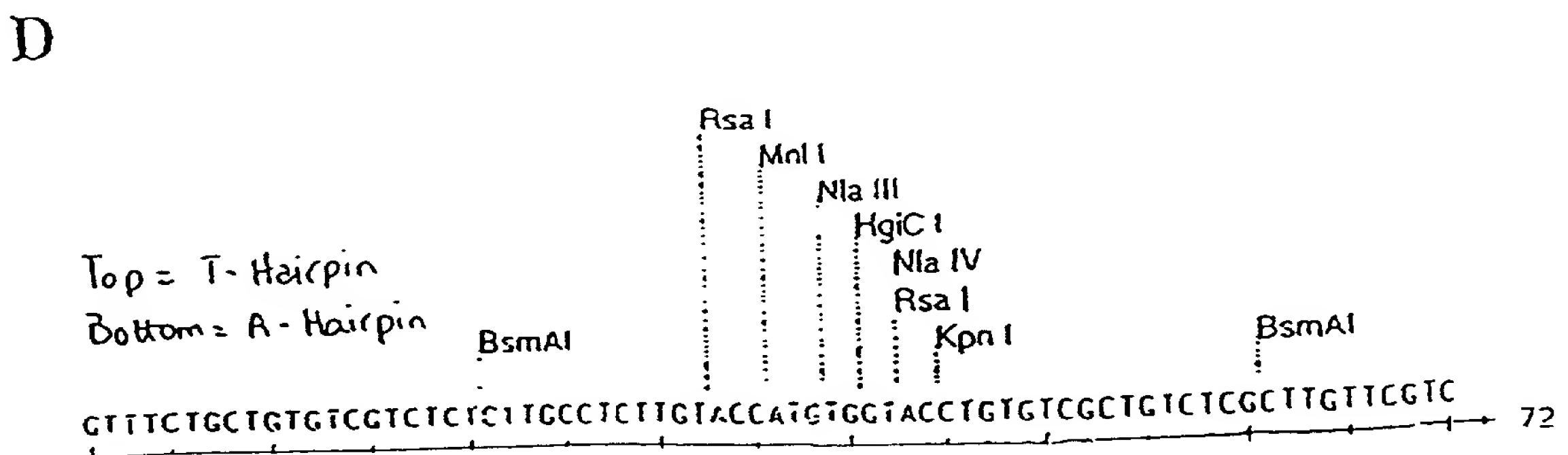
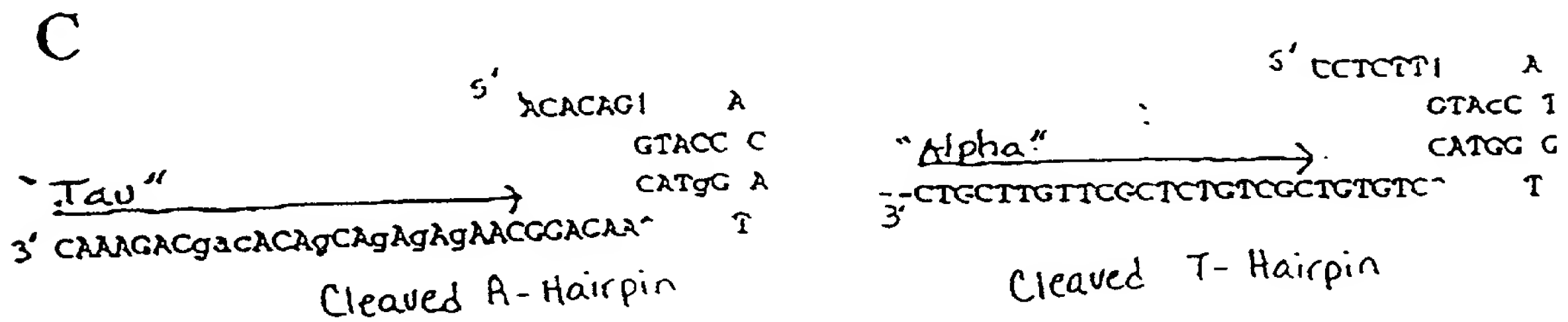


FIGURE 21



FIGURE 22A

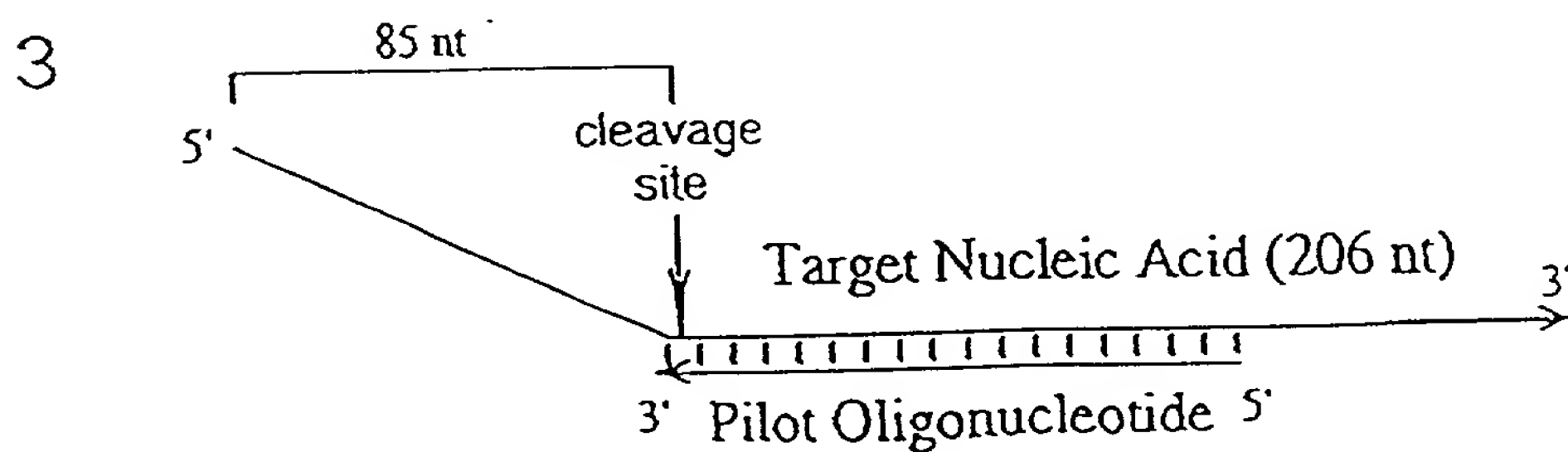
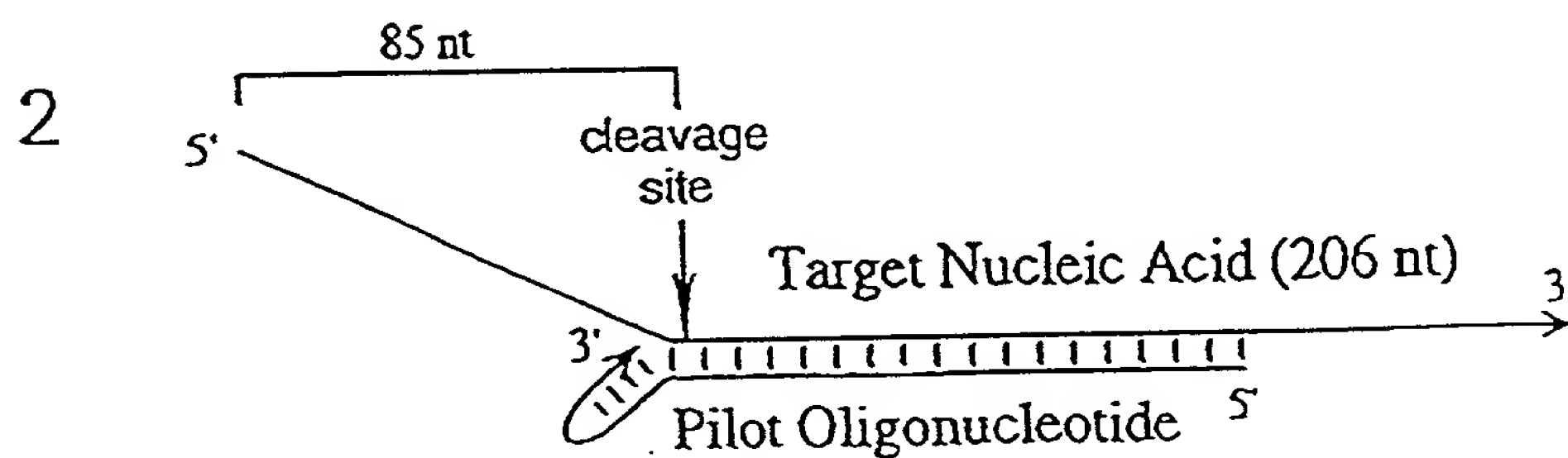
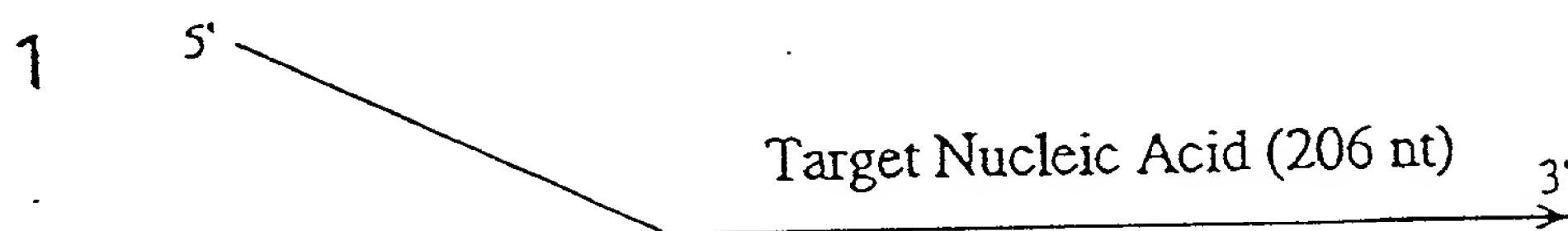


FIGURE 22B

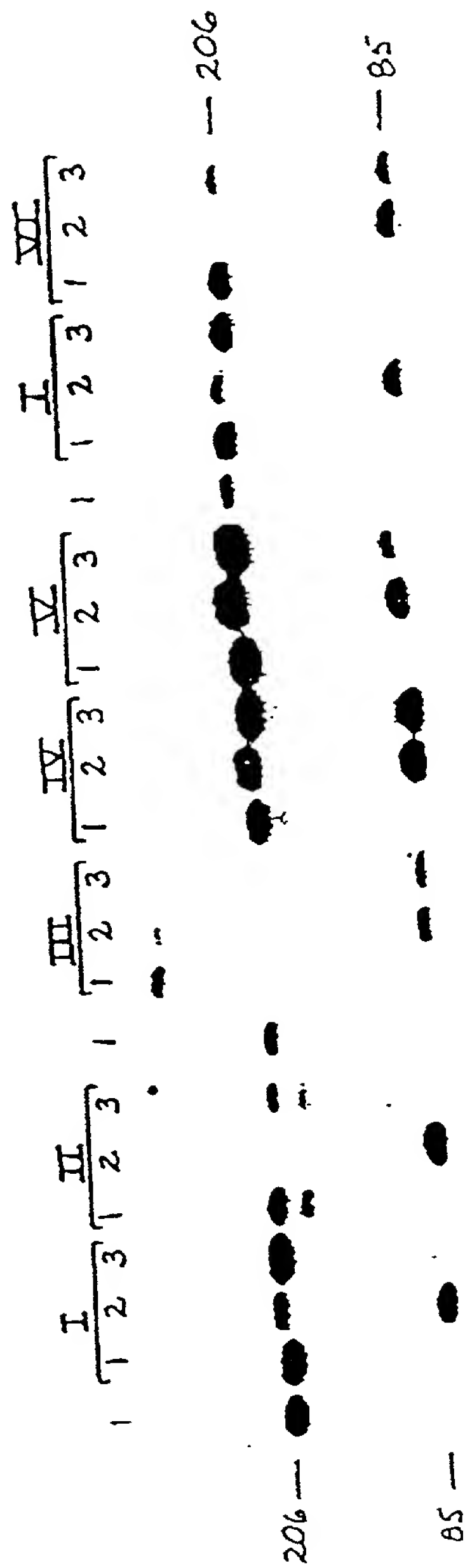


FIGURE 23

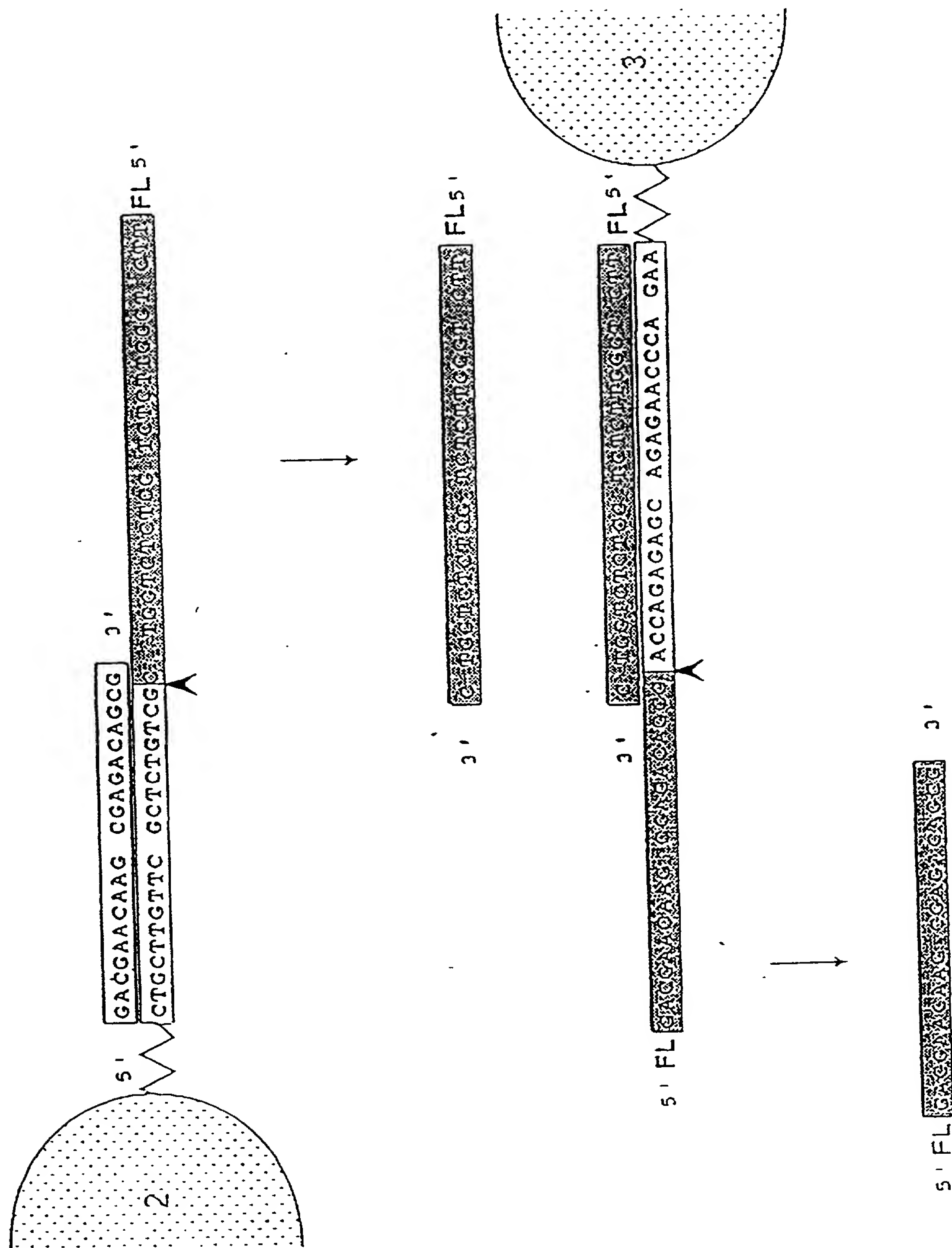
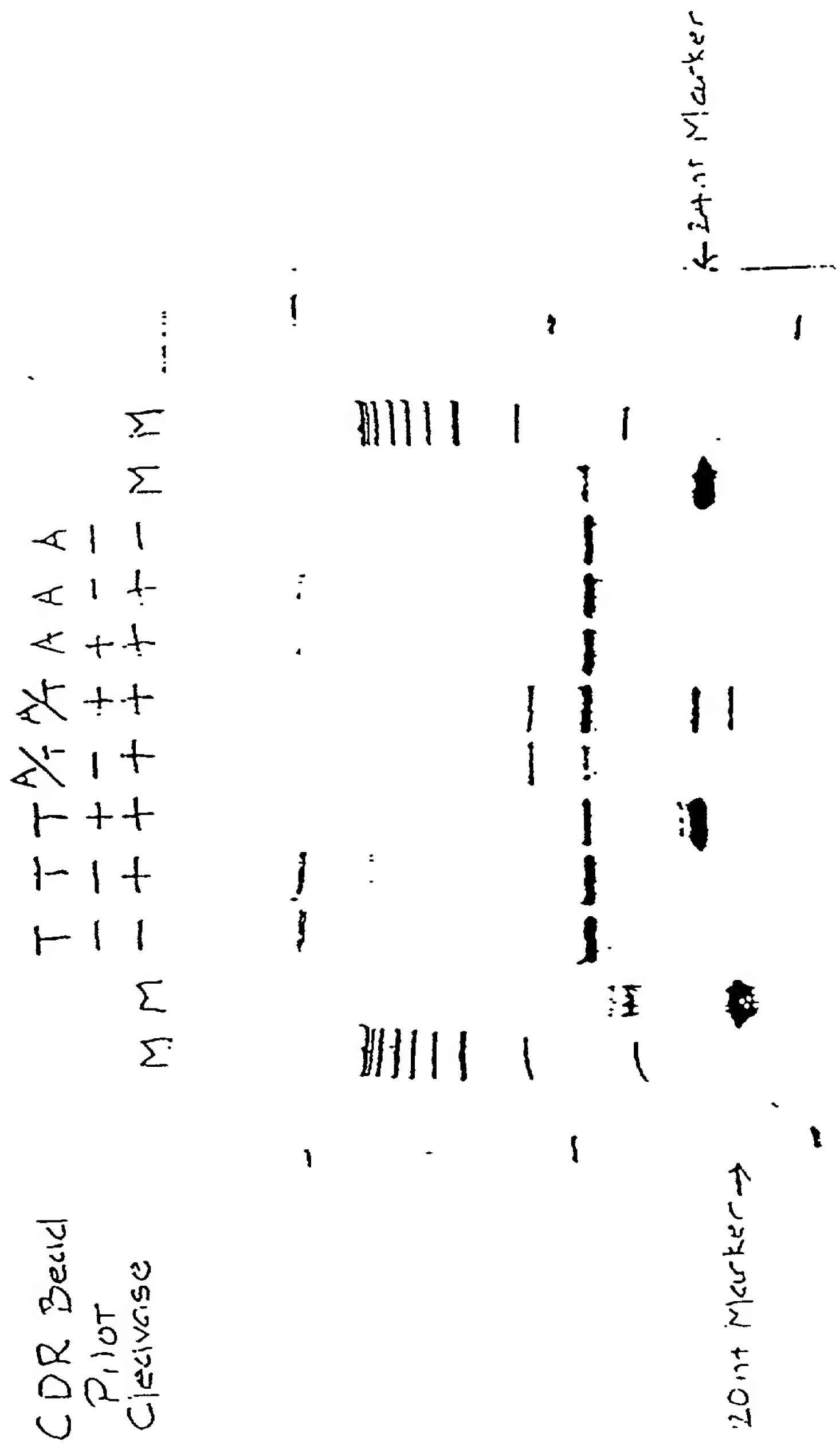


FIGURE 24



094093 000001

FIGURE 25

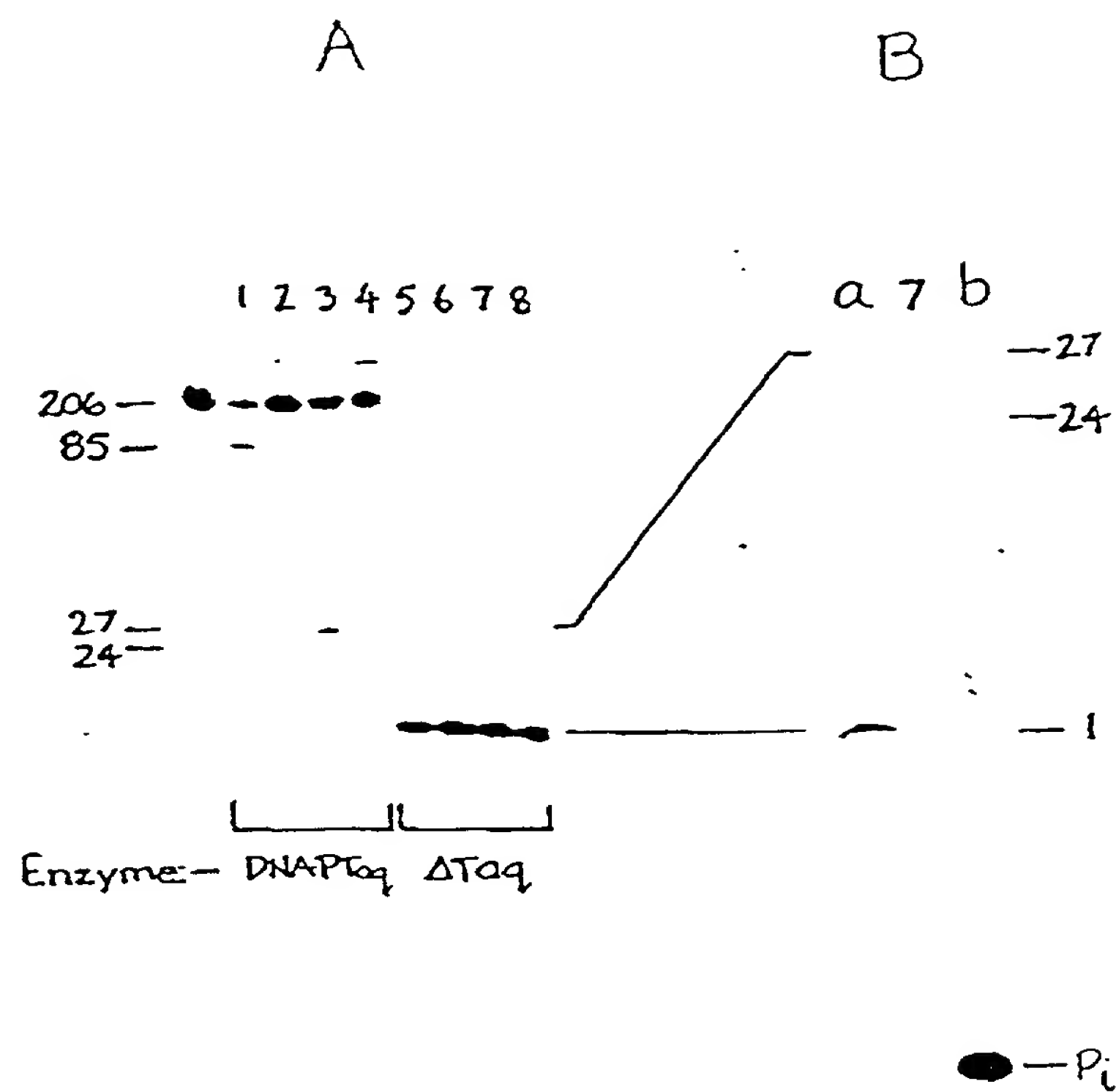
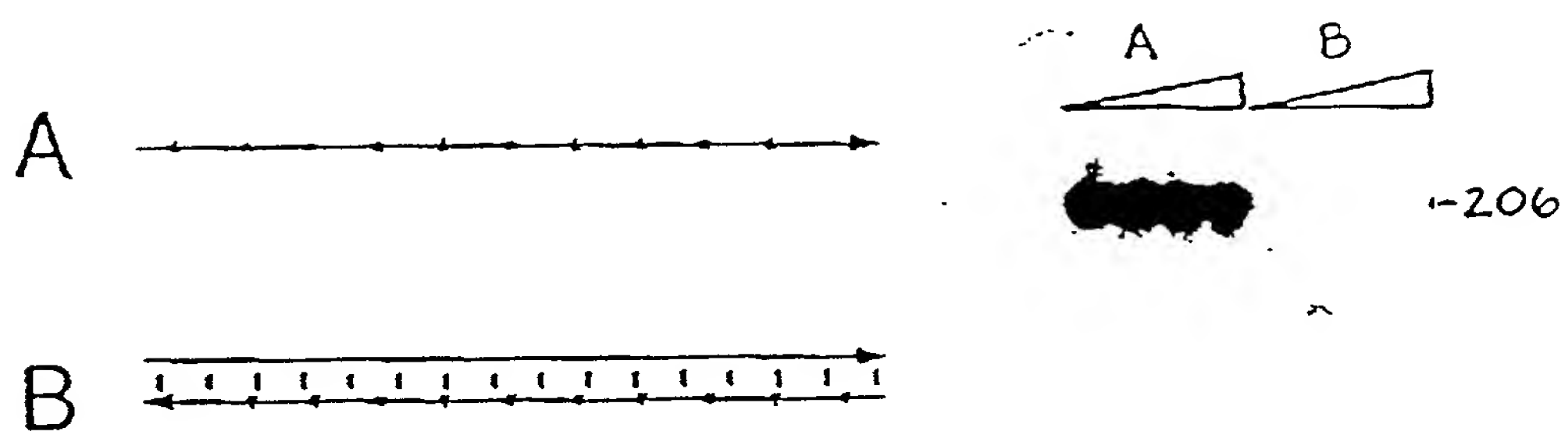


FIGURE 26



* = ^{32}P

FIGURE 27

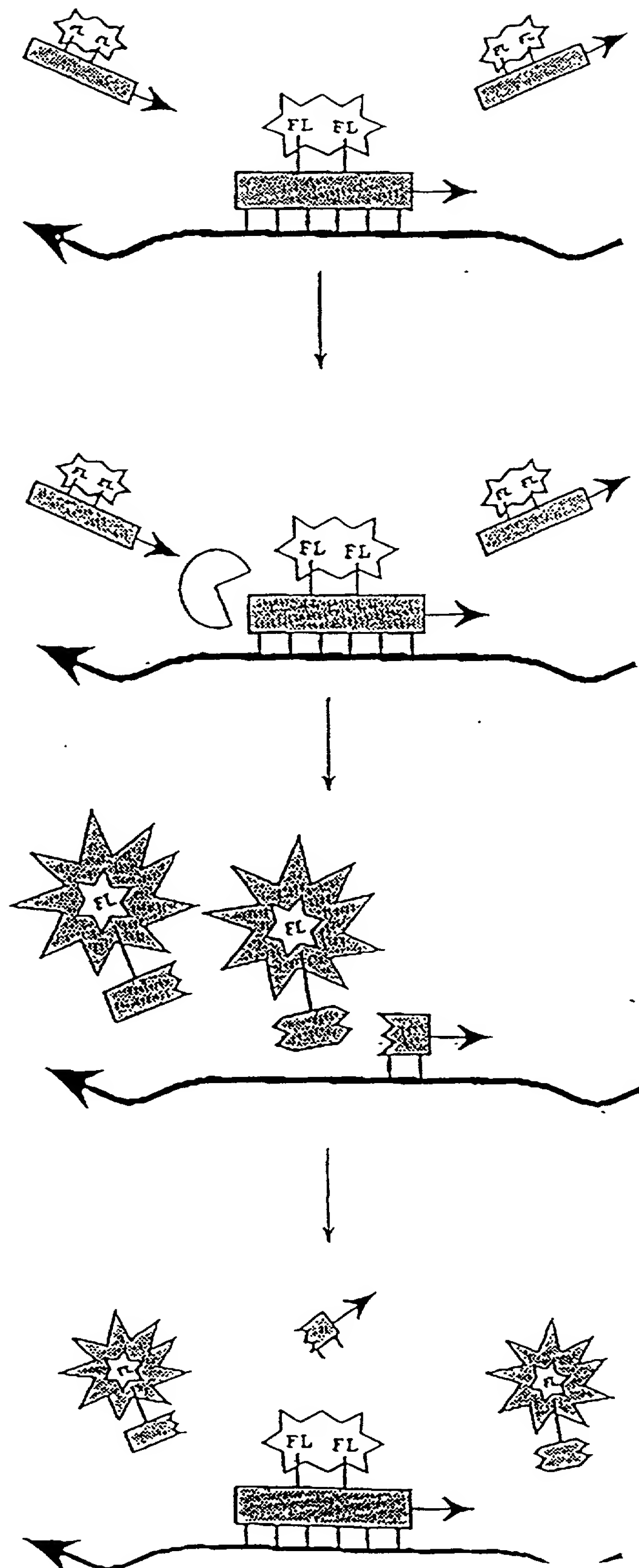
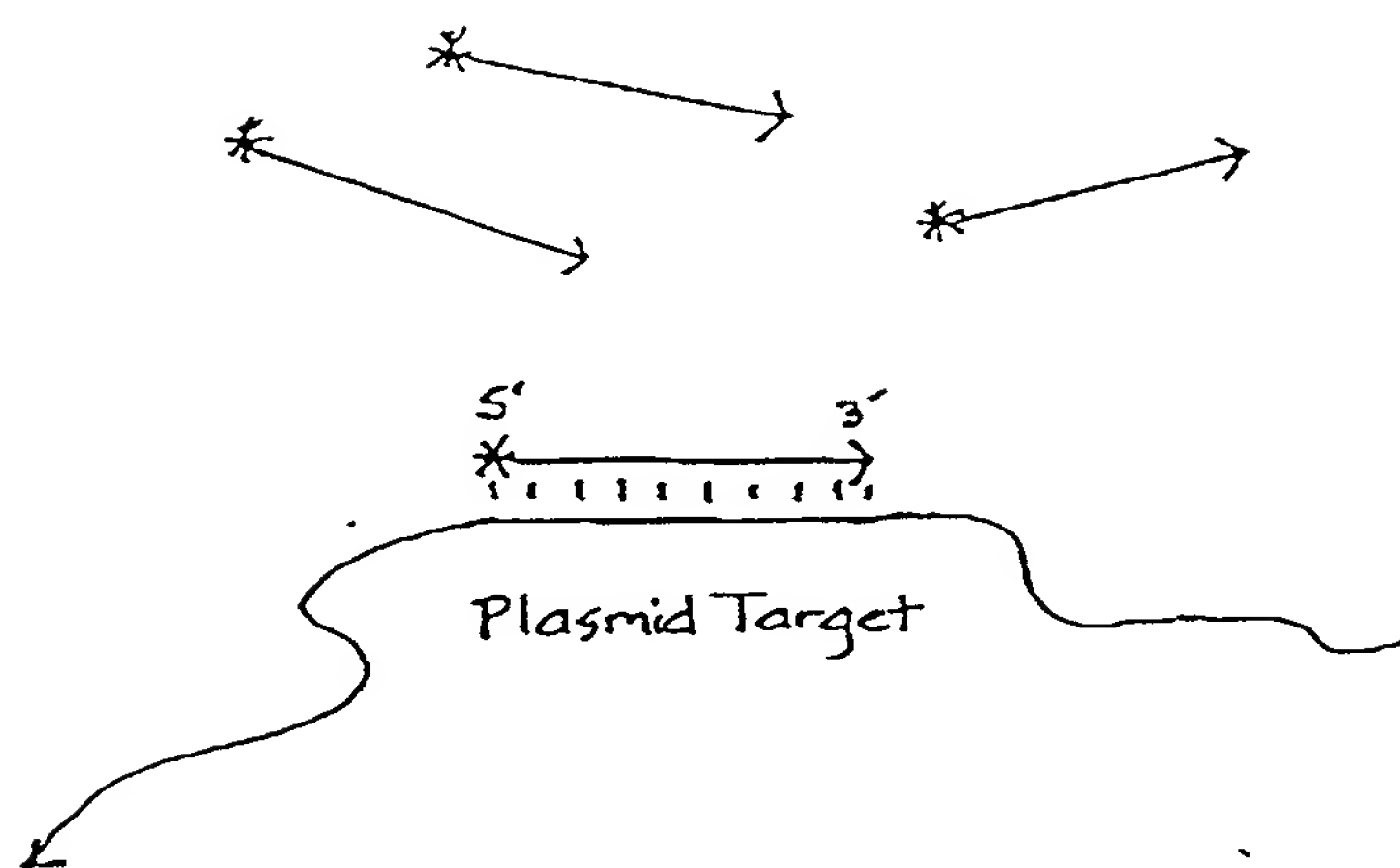


FIGURE 28A



* = ^{32}P 5' terminal phosphate

FIGURE 28B



FIGURE 29

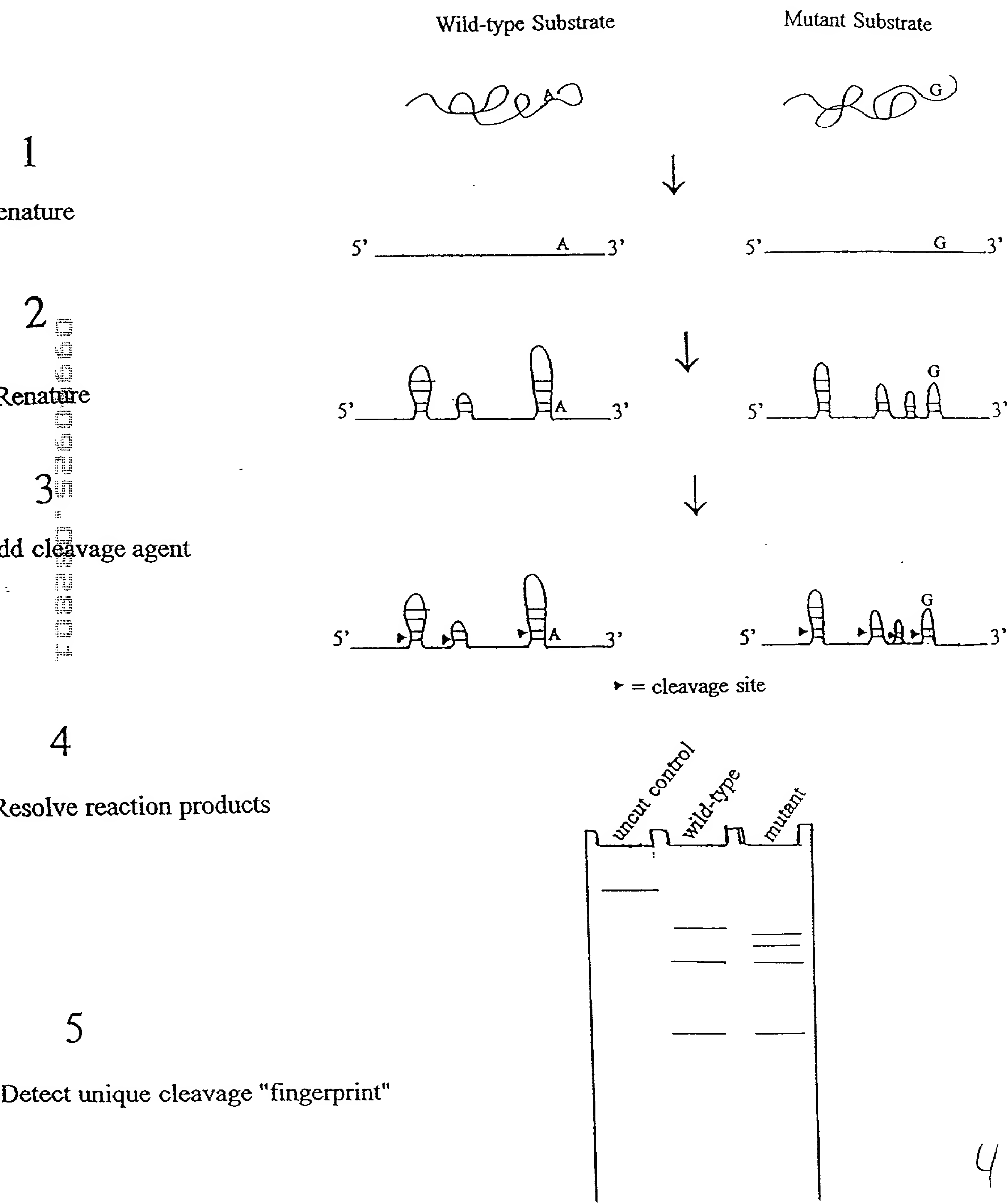


FIGURE 30

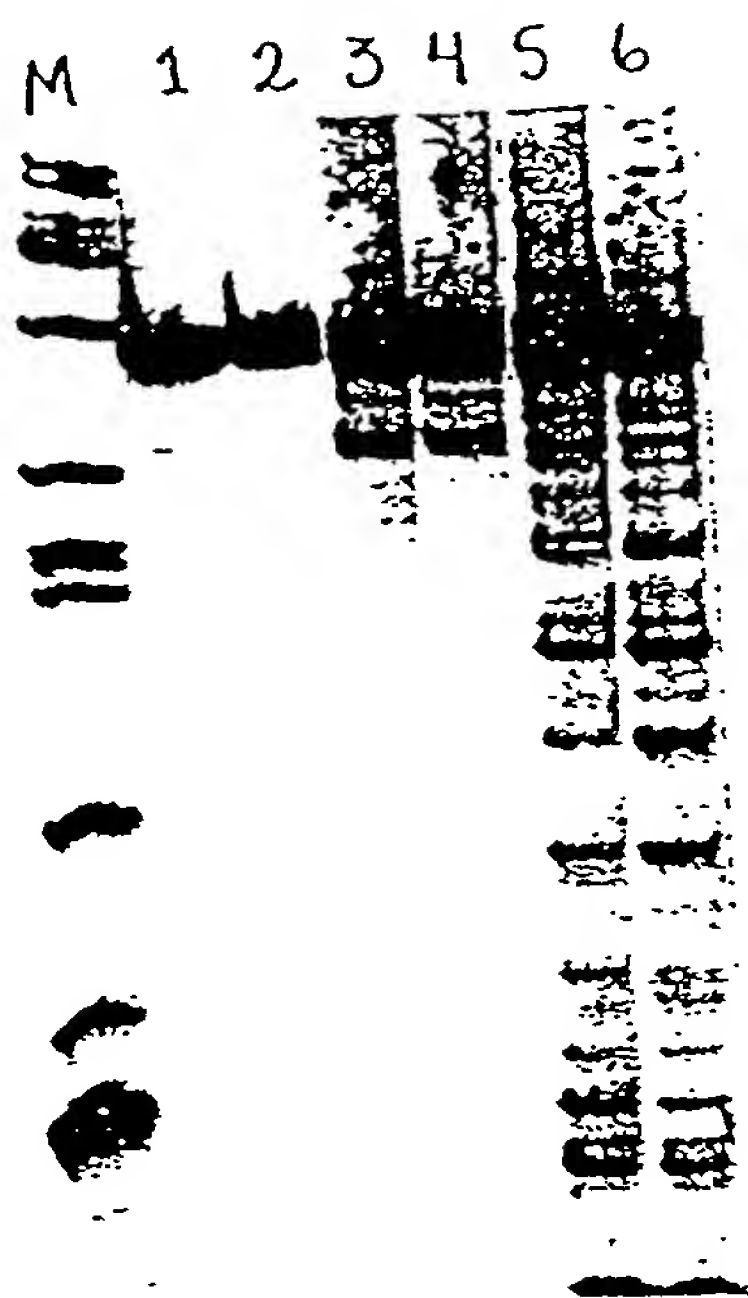


FIGURE 31

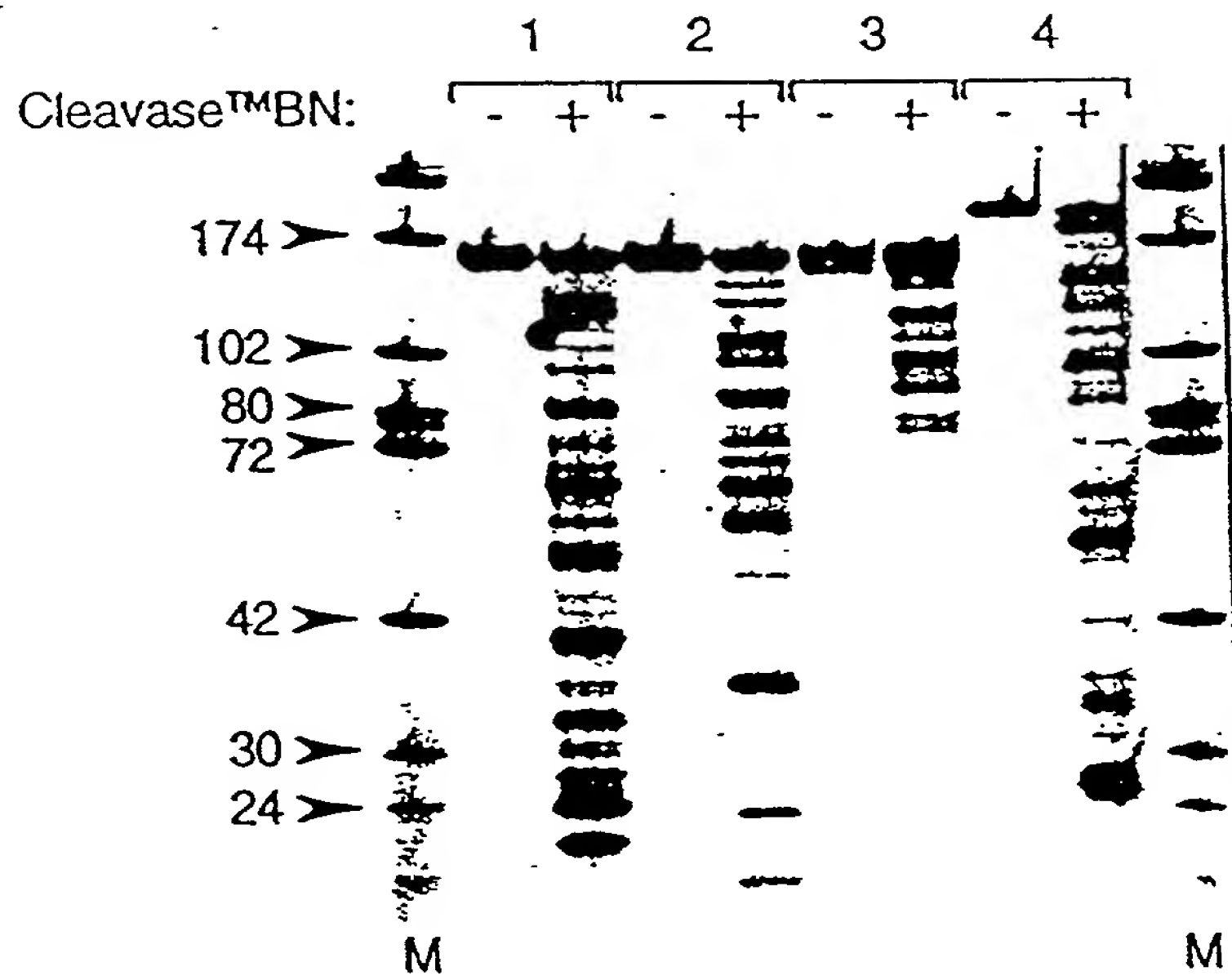
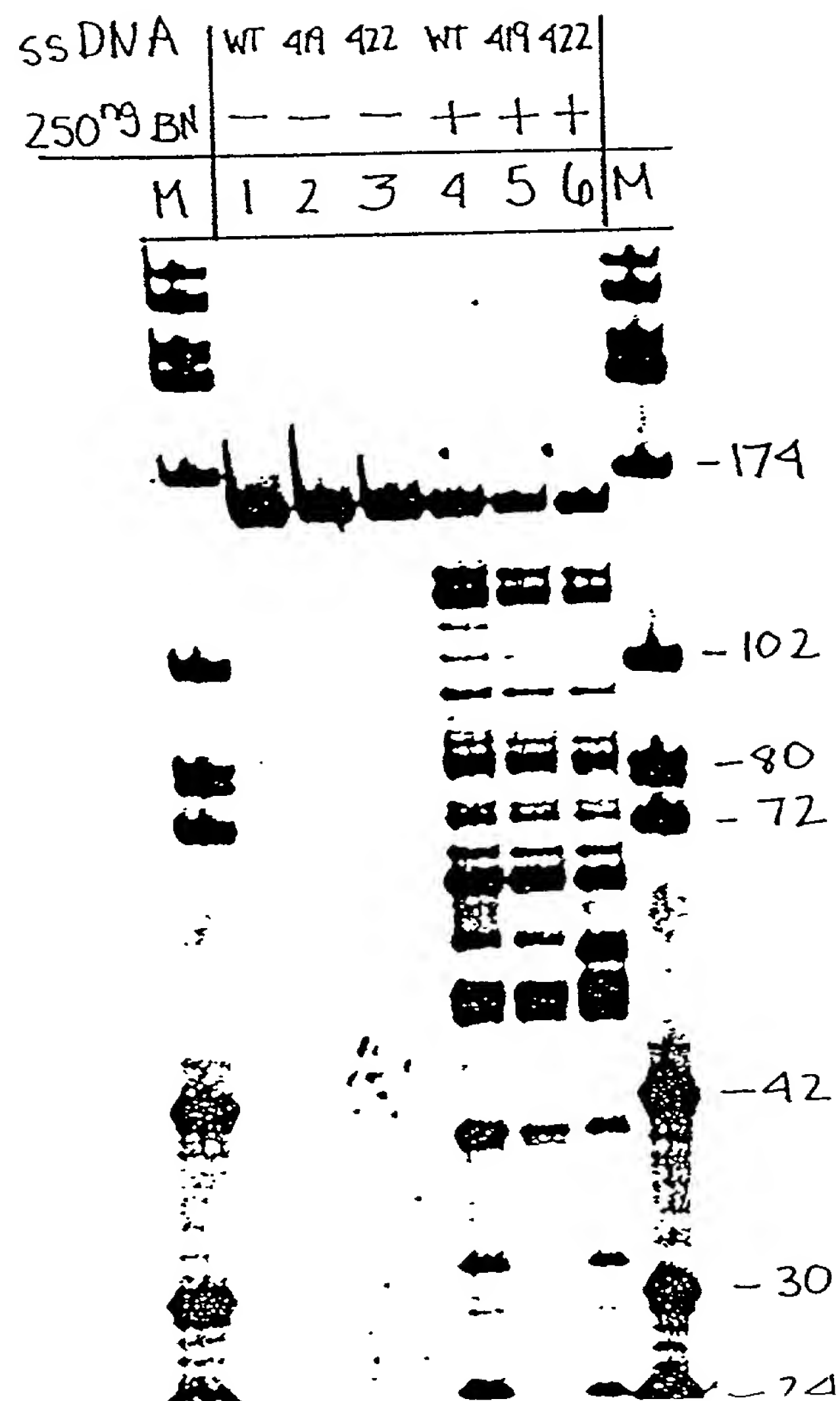
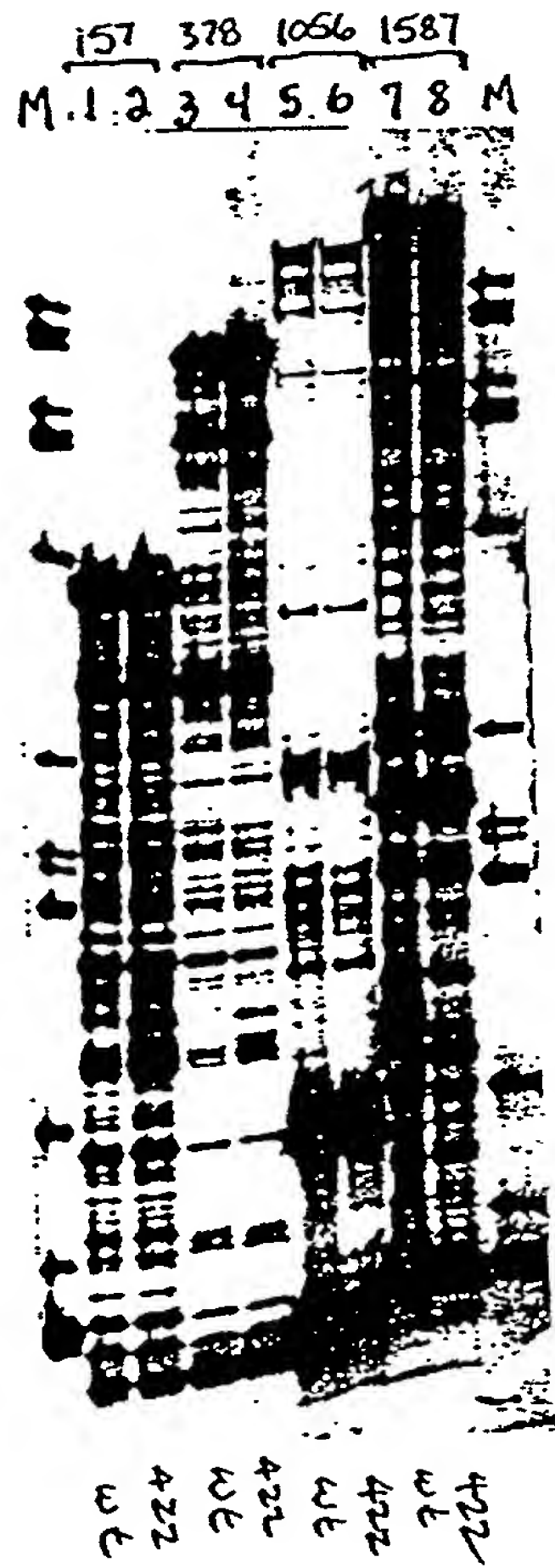


FIGURE 32



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FIGURE 33



1987	1986
1985	1984
1983	1982
1981	1980
1979	1978
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FIGURE 34

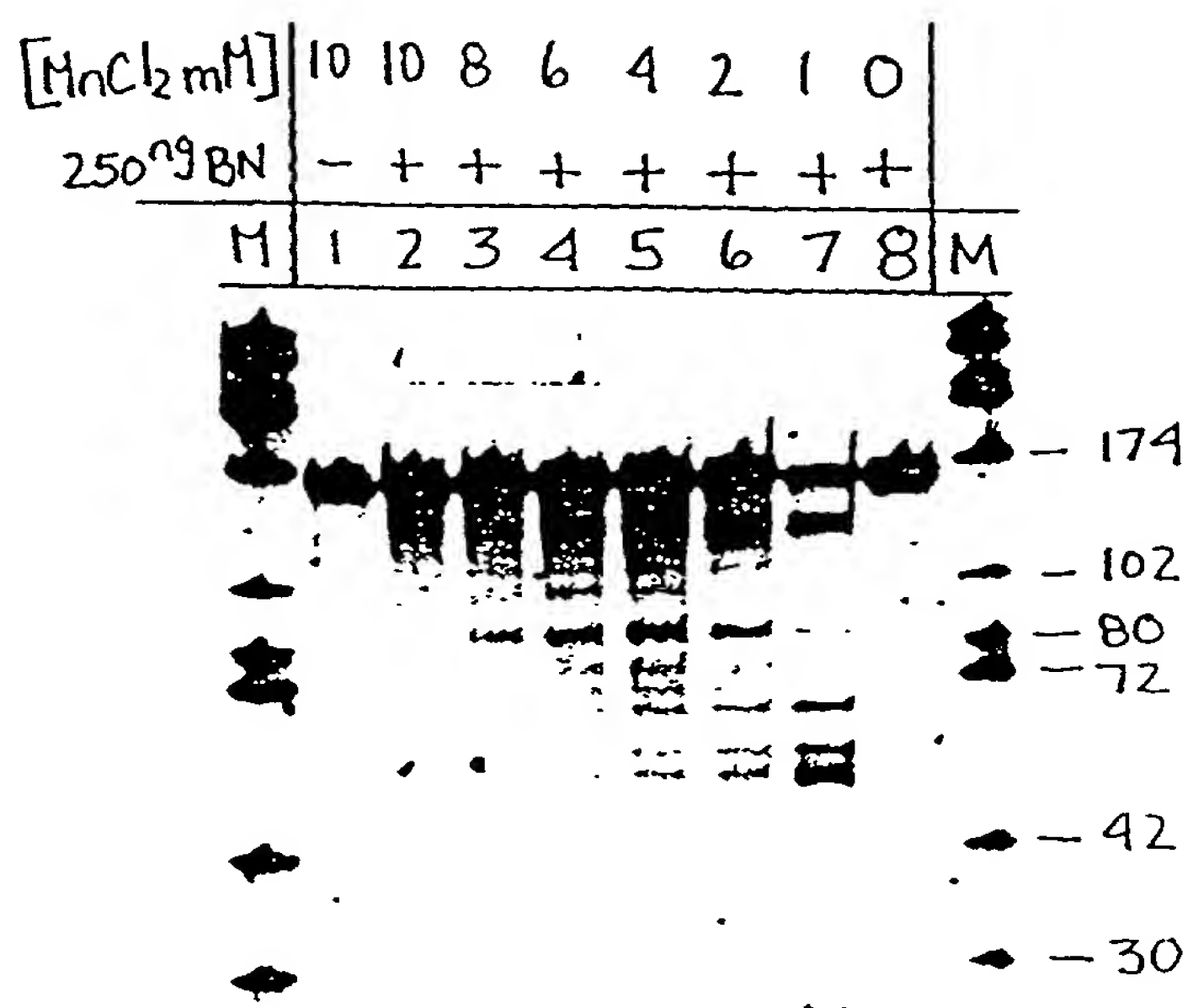


FIGURE 35

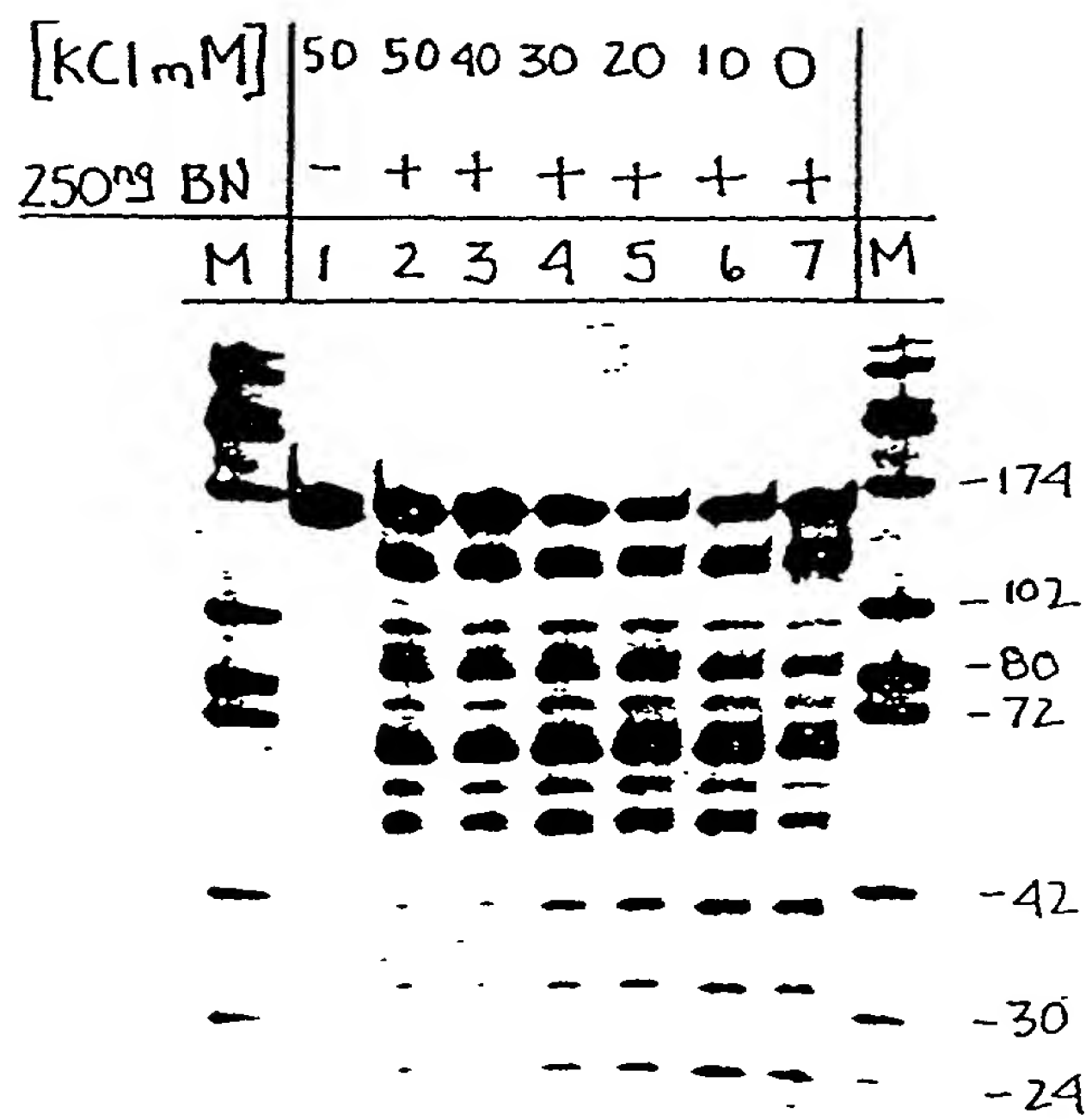


FIGURE 36

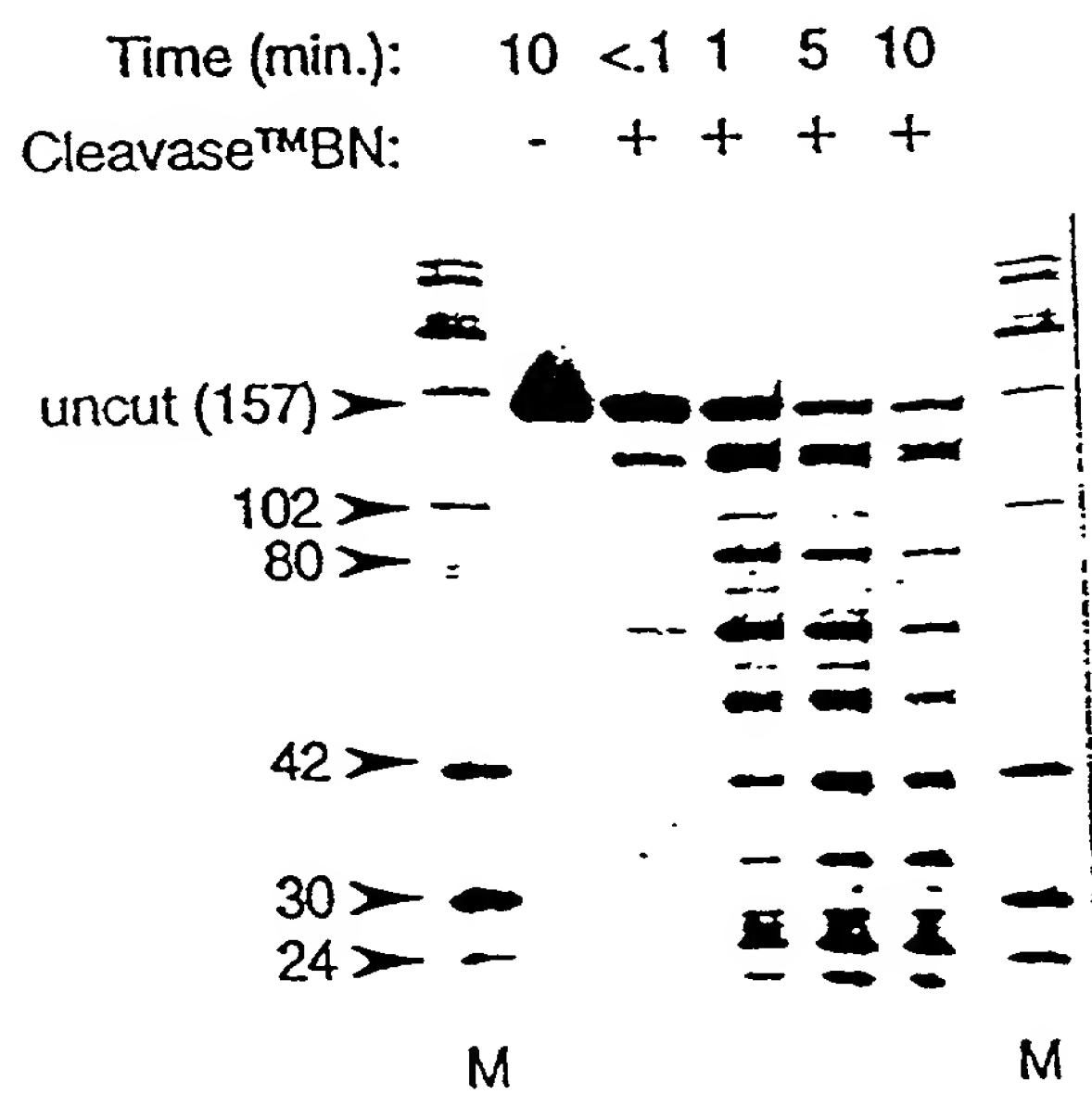
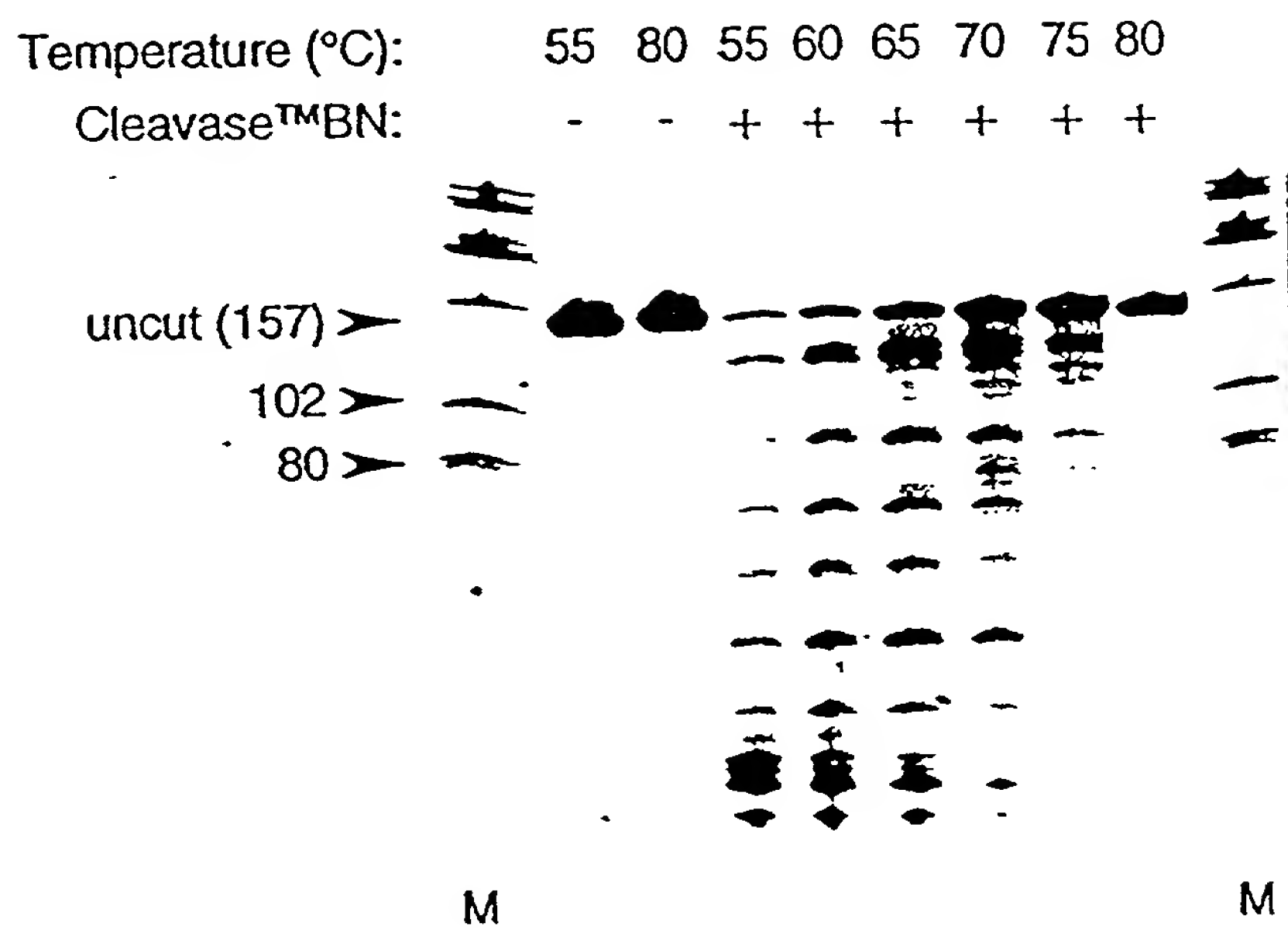


FIGURE 37



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03301-03301-03301

FIGURE 38

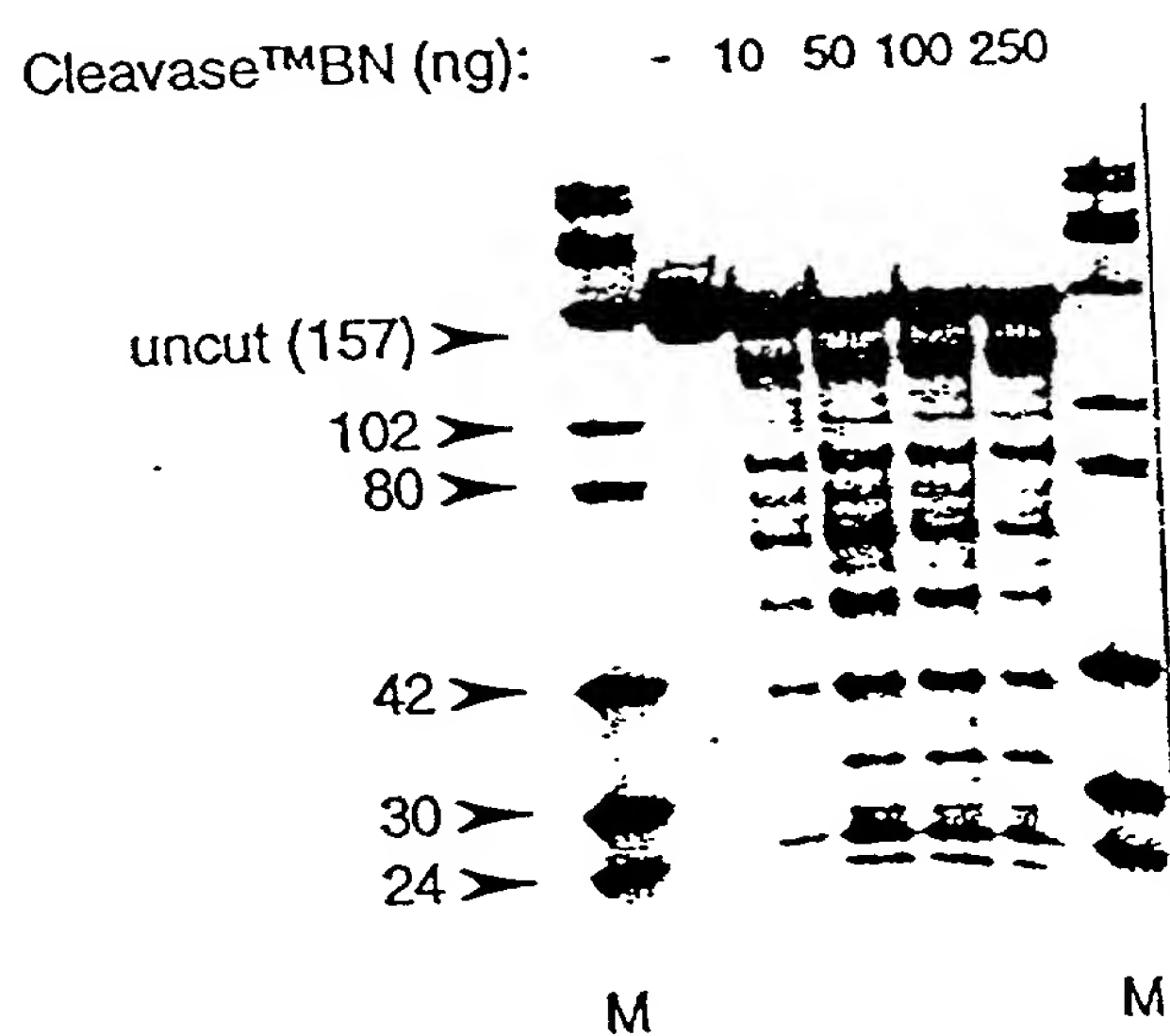


FIGURE 39

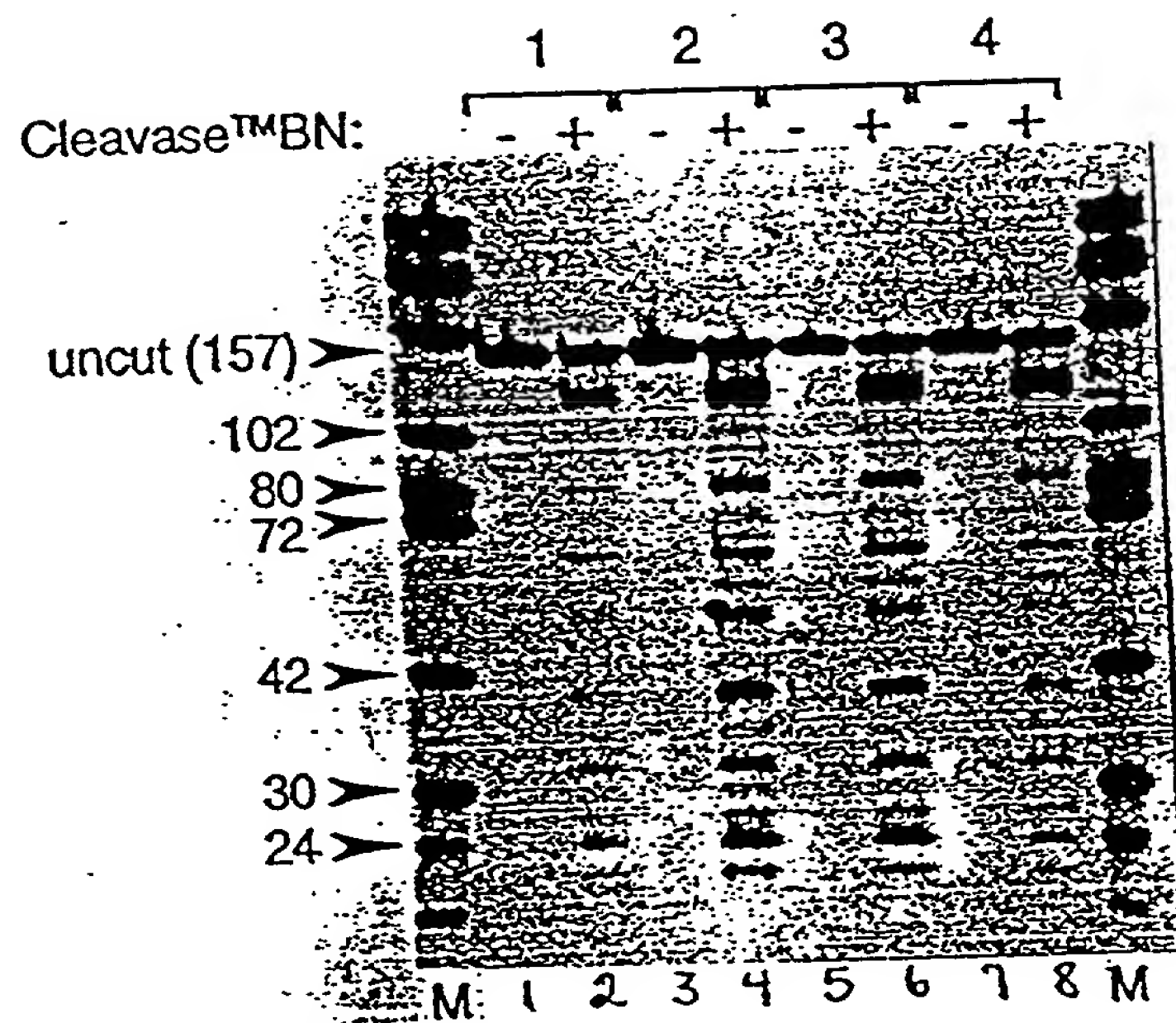


FIGURE 40

strand	5'-BIOTIN SENSE STRAND						5'-FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

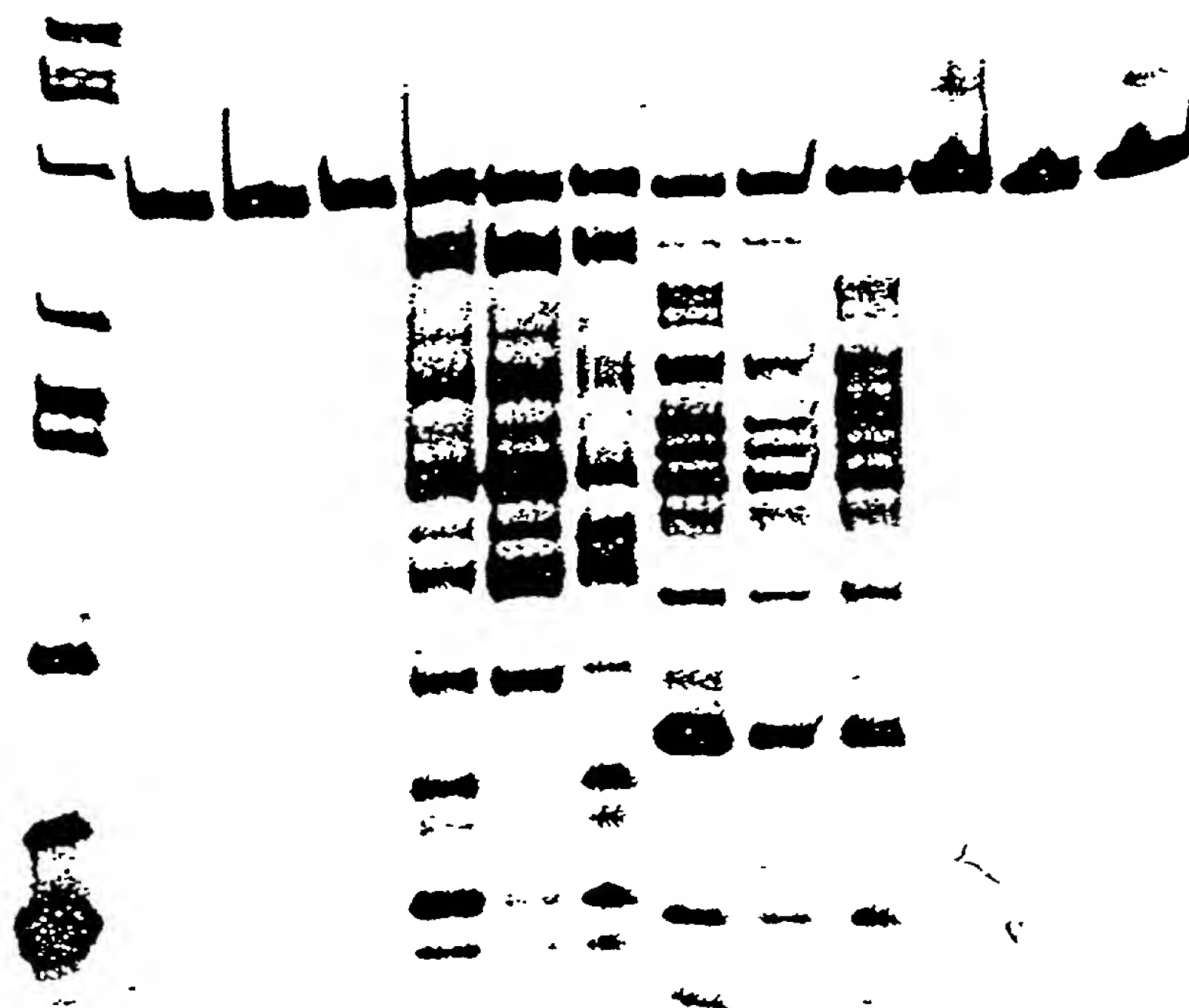


FIGURE 41

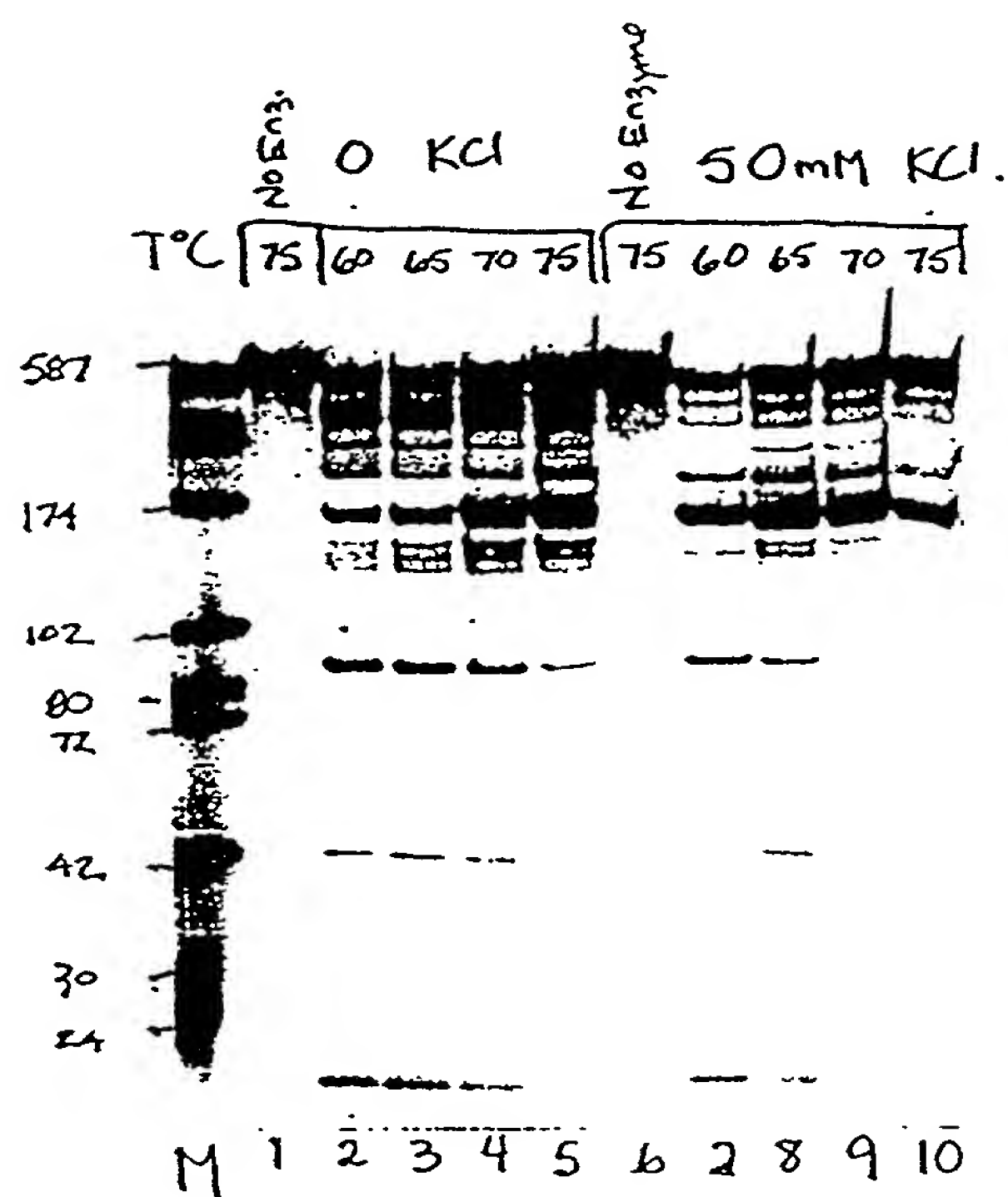


FIGURE 42

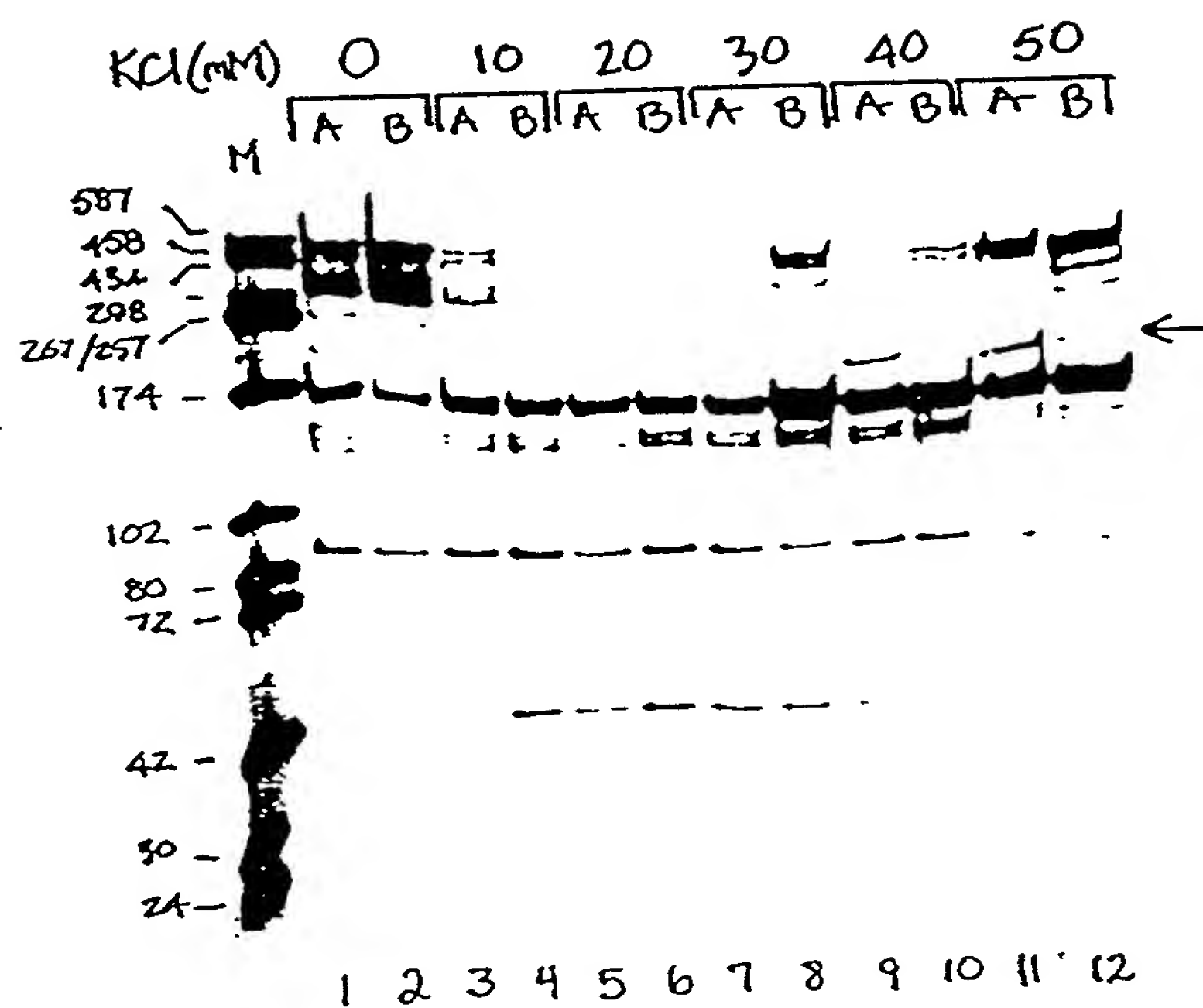
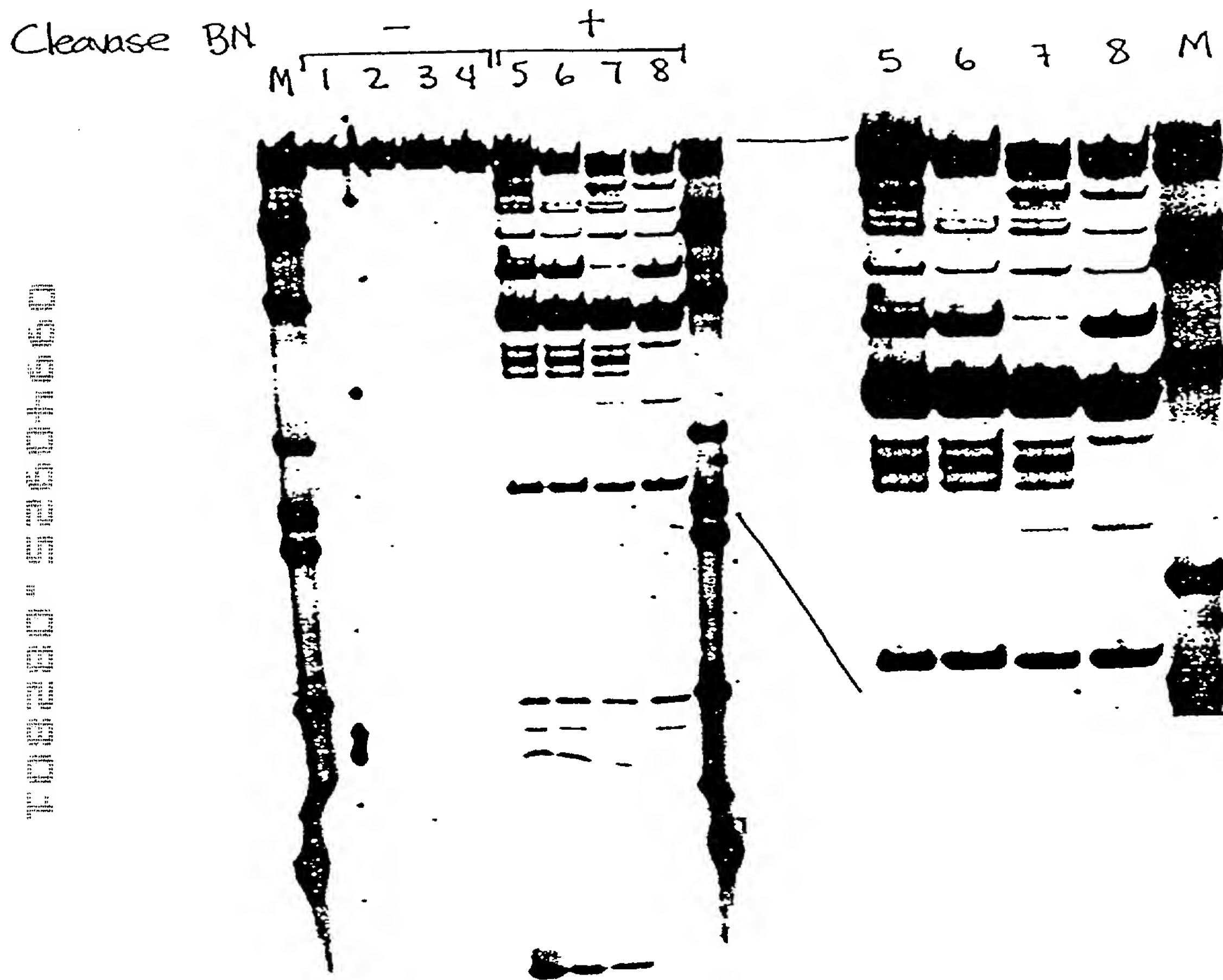


FIGURE 43



SS

FIGURE 44

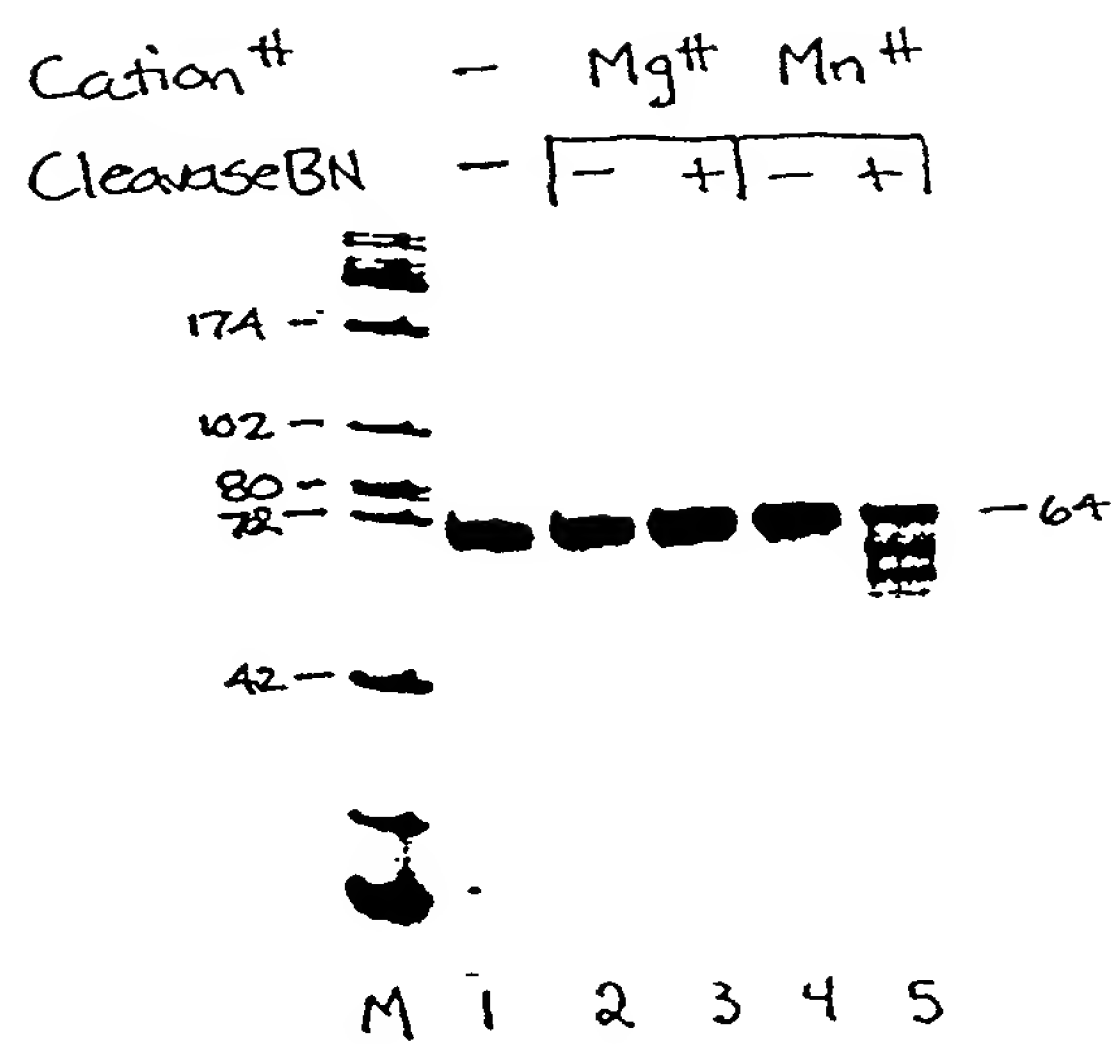
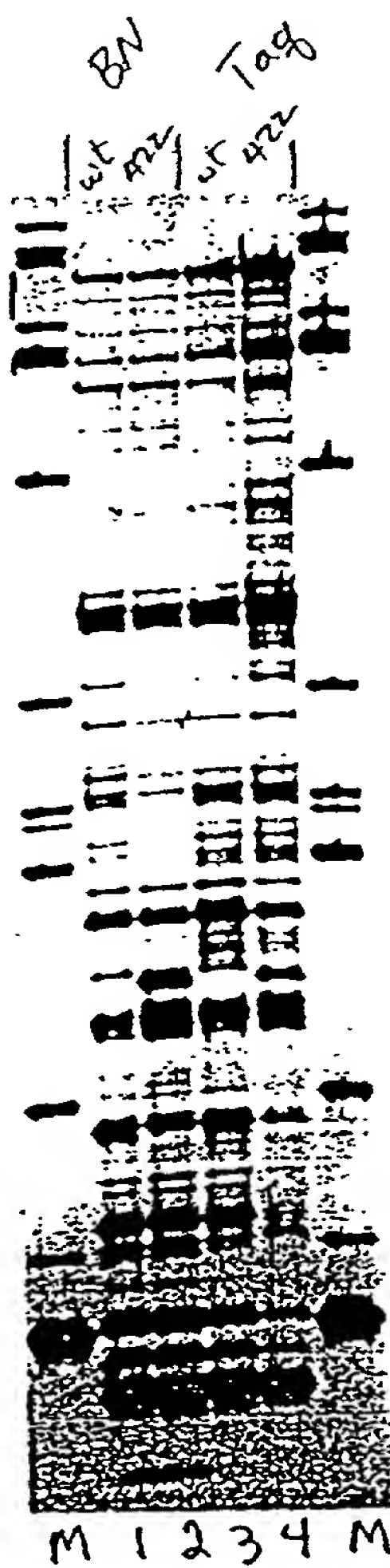


FIGURE 45



57

FIGURE 46

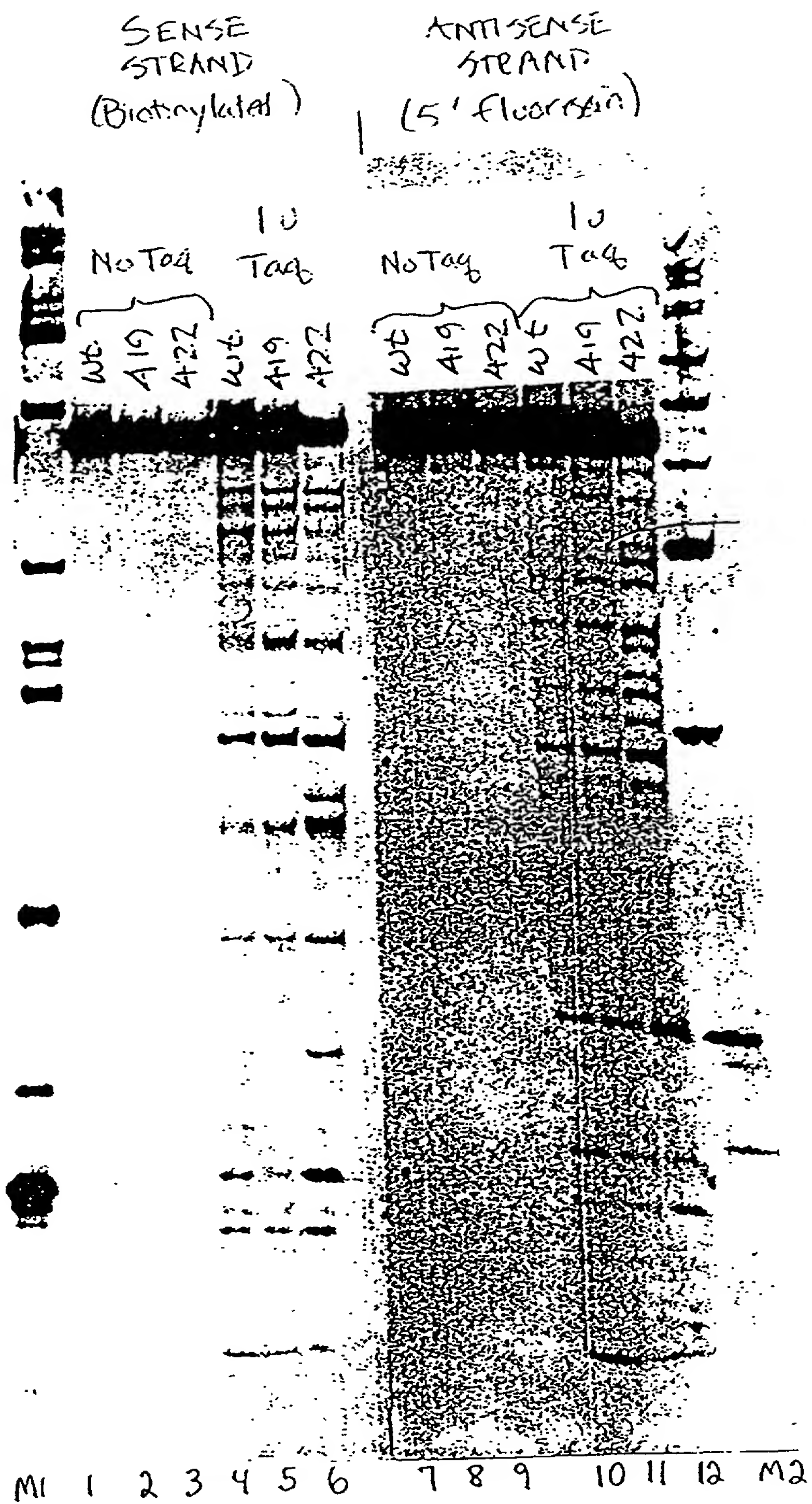
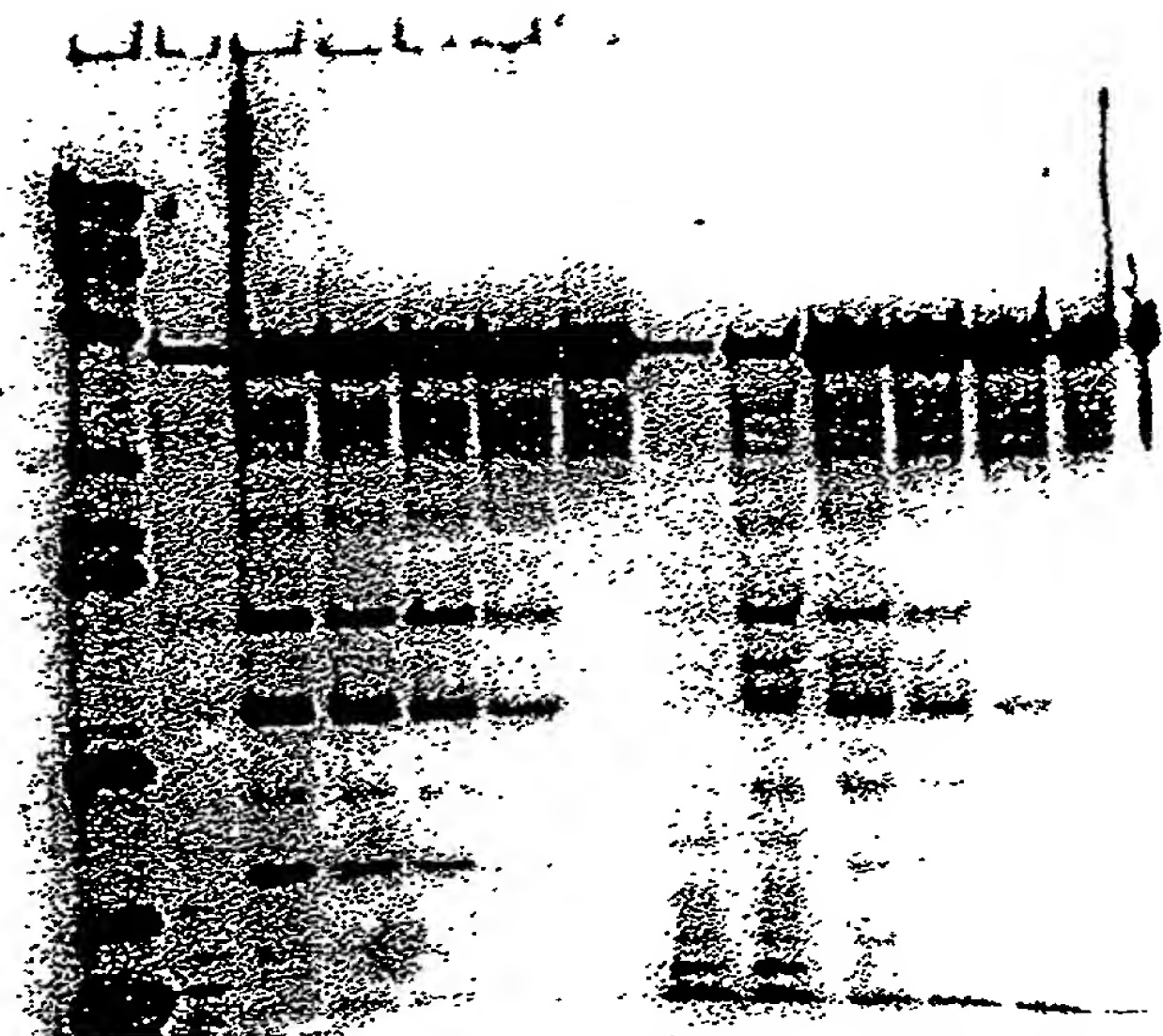


FIGURE 47

419

422

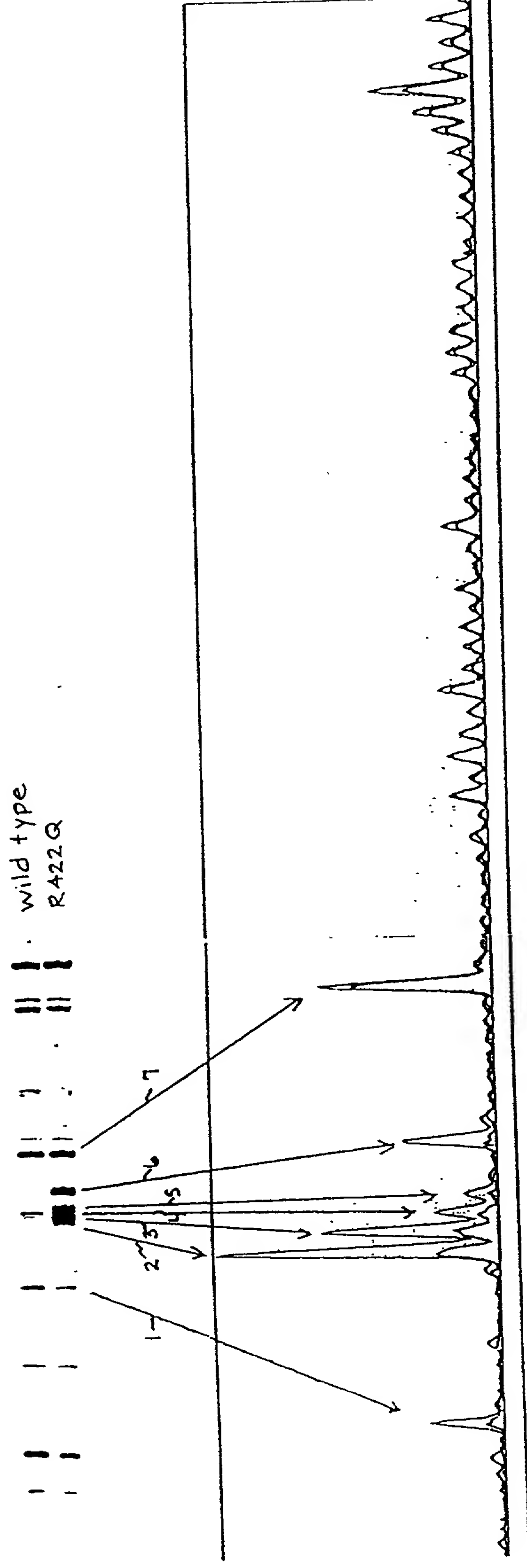
0.50	0.25	0.15	0.10	0.05	0.00	0.50	0.25	0.15	0.10	0.05	0.00
------	------	------	------	------	------	------	------	------	------	------	------



M 1 2 3 4 5 6 7 8 9 10 11 12

704230" 5260460

FIGURE 48
T08280" 52604650



100 8-1 5'GGCTGACAAGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG ATGTTACCGGGGAGCTACTGGGGAGGAGCCGGTCGGGAACGCCACTCTCT 100
3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTCTCGTCCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTCGCCAGCCCTTTCGGGGTGAGAGA
46.16-10 5'GGCTGACAAGAAACTCGCTGAGATAGCAGGACTTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
3'CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA
46.16-12 5'GGCTGACAAGAAACTCGCTGAGATAGCAGGACTTTCCACAAGGGG ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT
3'CCGACTGTTCTTCCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC TACAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA
19.16-3 5'GGCTGACAAGAAACTCGCTGAGACAGCAGGACTTTCCACAAGGGG ATGTTACGGGAGGTA CTGGGAGGAGCCGGTCGGGAACGCCCTCTCTCT
3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTTCCTCGCCAGCCCTTTCGGGTGAAAGA
CEM/251 5'CGCTGACAAGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG ATGTTACGGGAGGTA CTGGGAAAGGAGCCGGTCGGGAACGCCCTCTCTCT
3'CCGACTGTTCTTCCCTTTGAGCGACTTTGTCTGCTCCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTTCCTCGCCAGCCCTTTCGGGTGAAAGA
36.8-3 5'GGCTGACAAGAAACTCGCTGAGACAGCAGGACTTTCCACAAGGGG ATGTTACGGGAGGTA CTGGGAGGAGCCGGTCGGGAACGCCCTCTCTCT
3'CCGACTGTTCTTCCCTTTGAGCGACTCTGTCTGCTCCCTGAAAGGTGTTCCCC TACAATGCCCTCCATGACCCCTTCCTCGCCAGCCCTTTCGGGTGAGAGA
100.8-1 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG 200
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC
46.16-10 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC
46.16-12 5'TGGTGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC
19.16-3 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC
CEM/251 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC
36.8-3 5'TGATGTATAAATATCACTGCATTTCCGCTCTGTATTTCAGTCGGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGAGCGCCT CTCCGACCGTCTAACTCGGGAACCCCTCCAAGAGAGGTCGTGATCGTCCATC

61

L. 100.8-1 5' AGCCTGGGTGTTCCCTGCTAGACTCTACACGACACTTGGCCGGTCTGG CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 76) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

L. 46.16-10 5' AGCCTGGGTGTTCCCTGCTAGACTCTACACGACACTTAGCCAGTGTGGG CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 77) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAATCGGTACGACCC GTCTCACCGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

L. 46.16-12 5' AGCCTGGGTGTTCCCTGCTAGACTCTACACGACACTTGGCCAGTGTGGG CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 78) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGTACGACCC GTCTCACCGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

L. 19.16-3 5' AGCCTGGGTGTTCCCTGCTAGACTCTACACGACACTTGGCCGGTGTGGG CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 79) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

L. CEM/251 5' AGCCTGGGTGTTCCCTGCTAGACTCTACACGACACTTGGCCGGTGTGGG CAGAGTGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 80) 3' TCGGACCCACAAGGACGATCTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCACCTGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

L. 36.8-3 5' AGCCTGAGTGTCCCTGCTAAACTCTCACCAGCAGTGTGGCCGGTGTGGG CAGAGCGGCTCCACGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC
(seq ID N0: 81) 3' TCGGACTCACAAAGGACGATTTGAGAGTGGTCTGTAACCGGCCACGACCC GTCTCGCGGAGGTGCGAACGAAATTTCTGGAGAGTTATTTTCGACGG

← Hairpin →

350

L. 100.8-1 5' ATTTTAGAAGTAGCCAGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATCCGGTTCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

L. 46.16-10 5' ATTTTAGAAGTAAGCCAGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATTCGGTTCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

L. 46.16-12 5' ATTTTAGAAGTAAGCCAGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATTCGGTTCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

L. 19.16-3 5' ATTTTAGAAGTAGGCTAGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATCCGATCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

L. CEM/251 5' ATTTTAGAAGTAGTGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATTCGATCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

L. 36.8-3 5' ATTTTAGAAGTAGGCTAGTGTGTGTCCCATCTCTCCTAGCCGCGCCTG G 3'
3' TAAATCTTCATCCGATCACACACAAAGGTAGAGAGGATCGGCGCGGAC C 5'

62

FIGURE 50

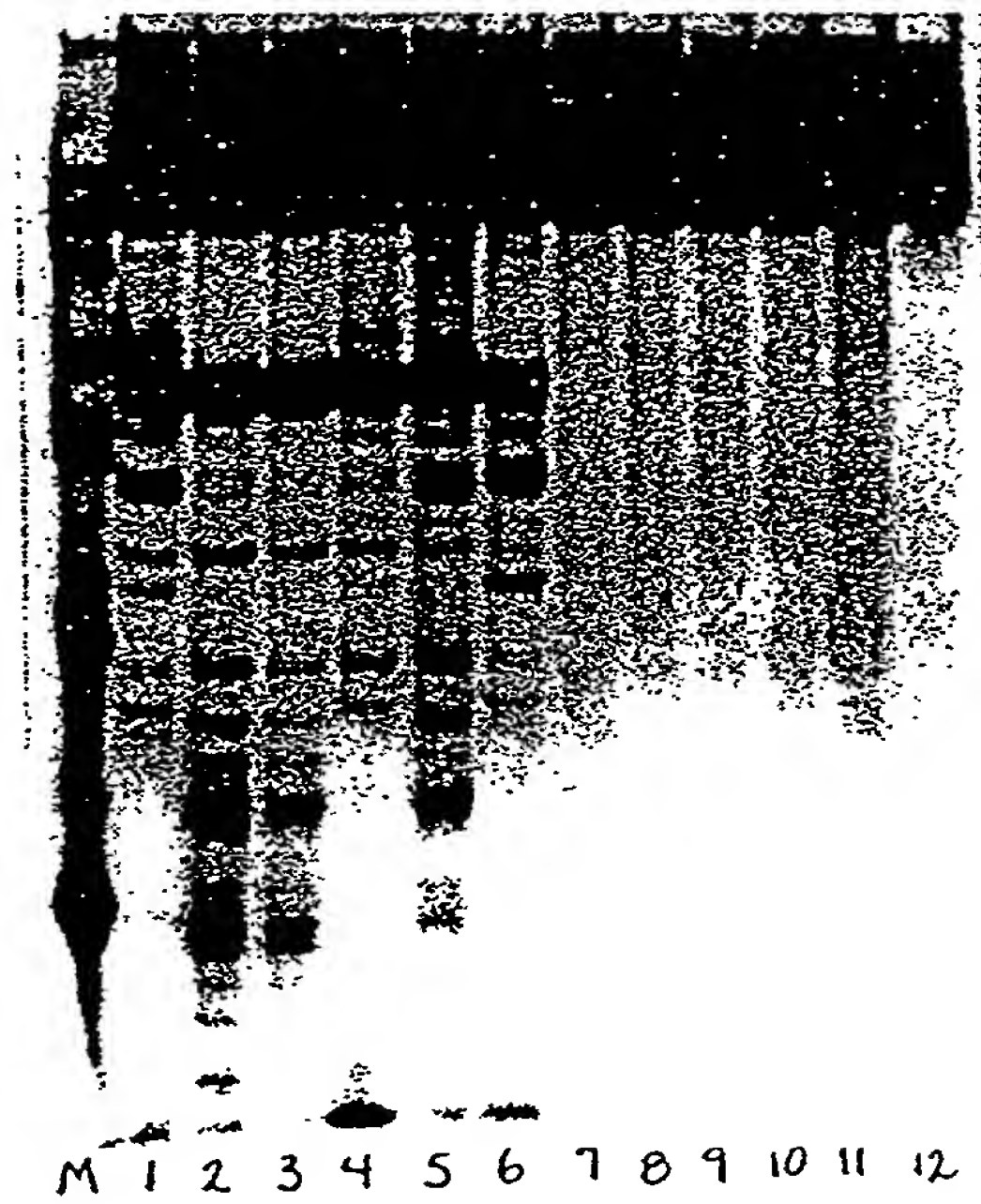
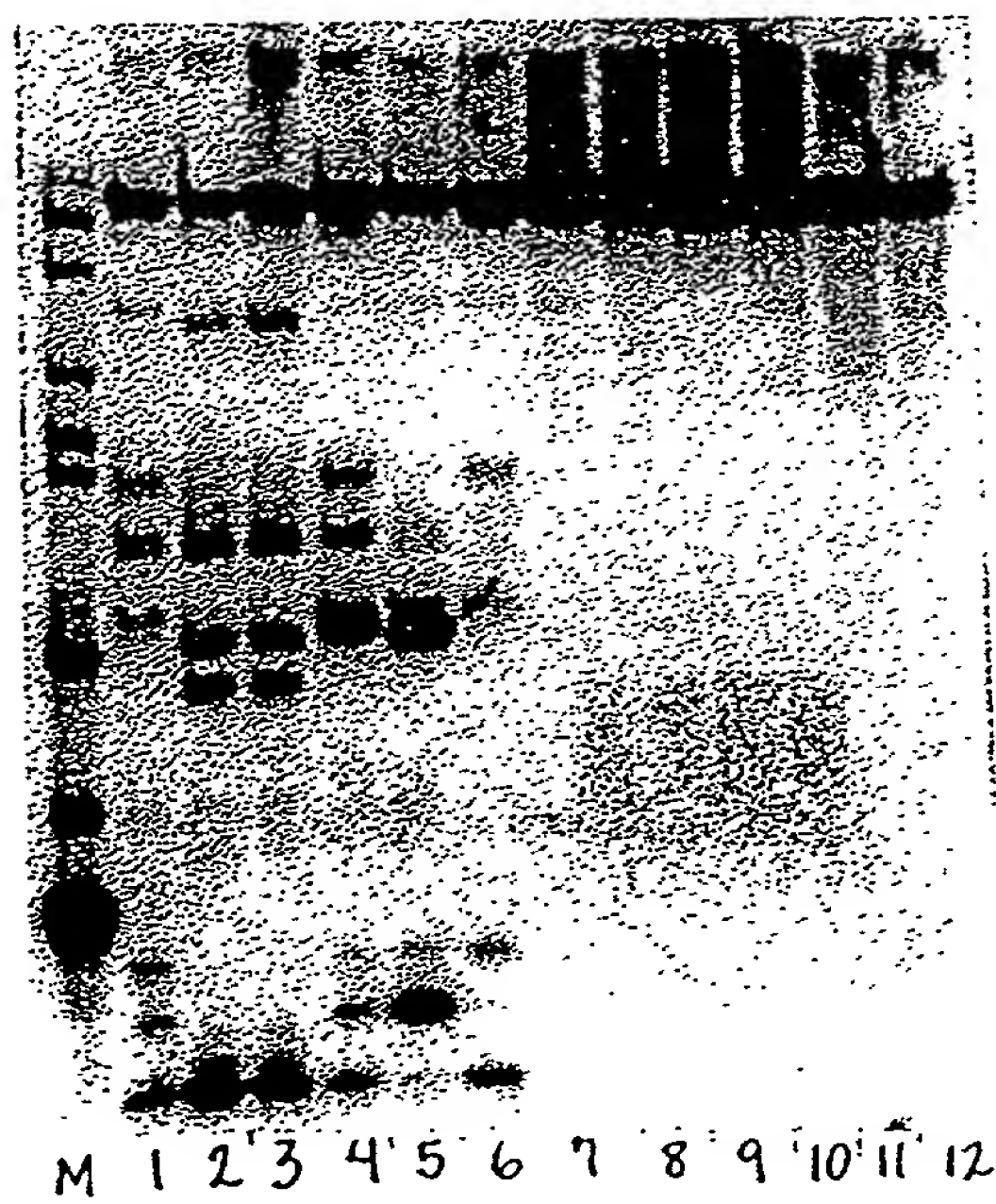
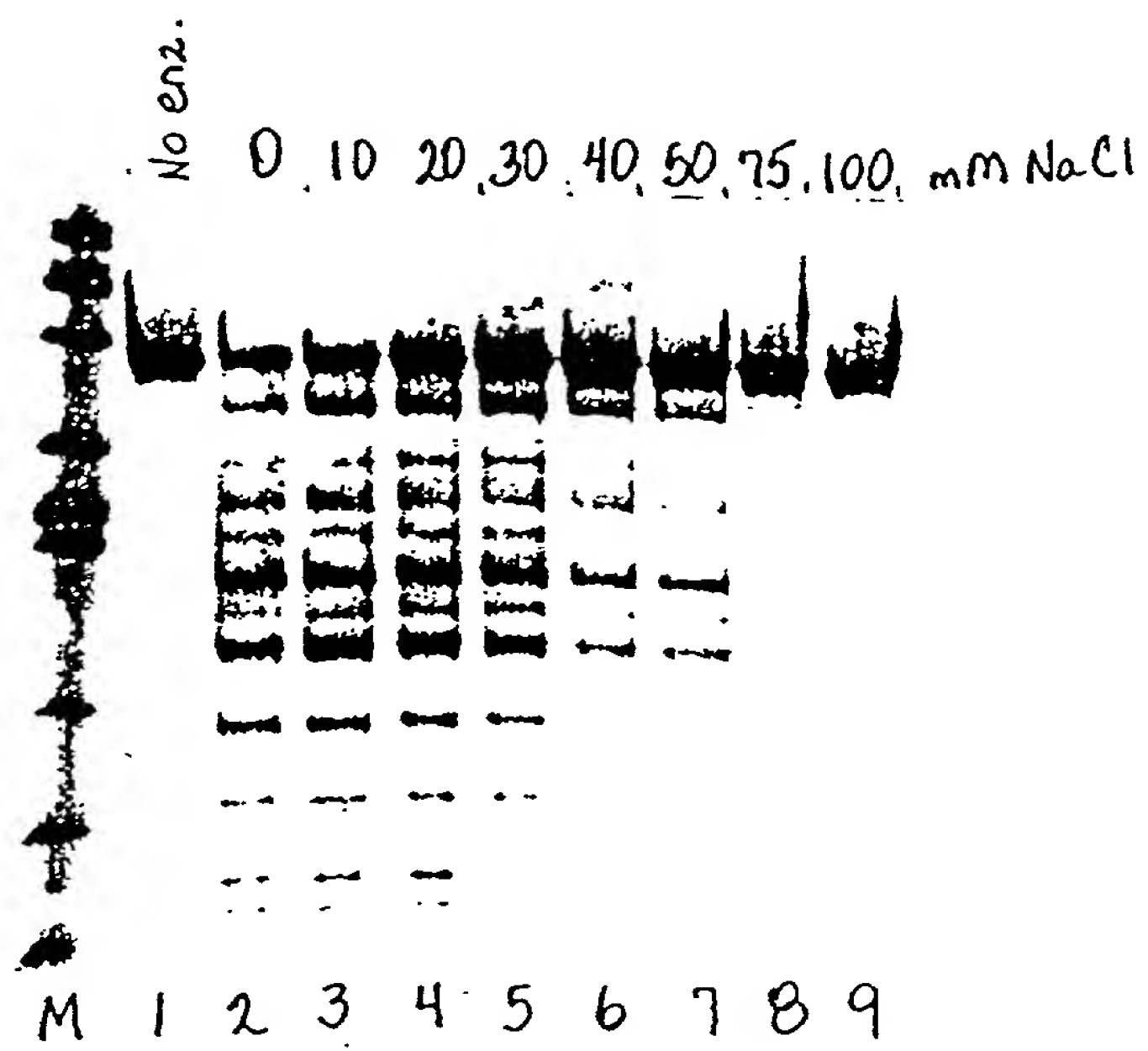


FIGURE 51



TOP230" 52504650

FIGURE 52



65

FIGURE 53

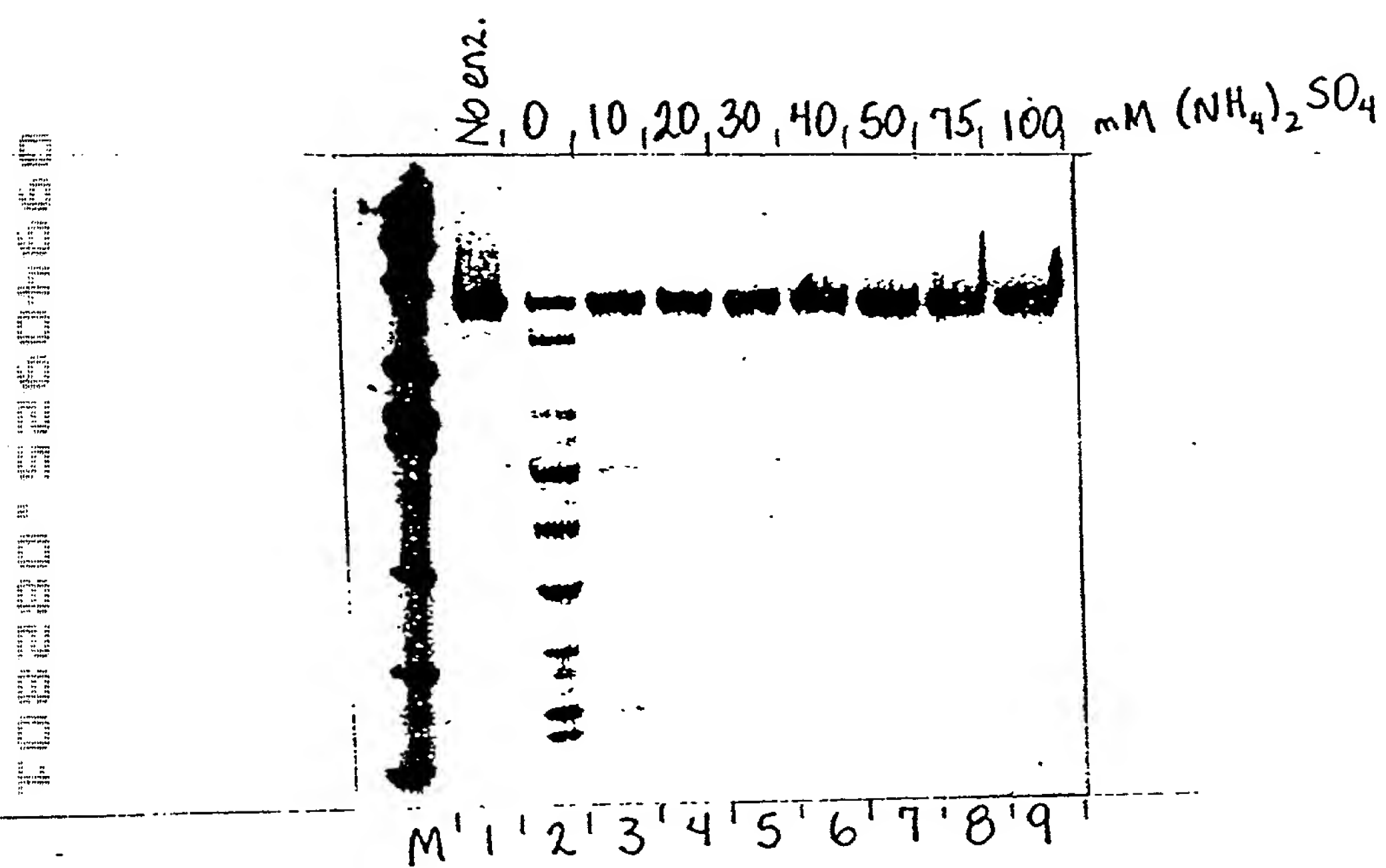


FIGURE 54

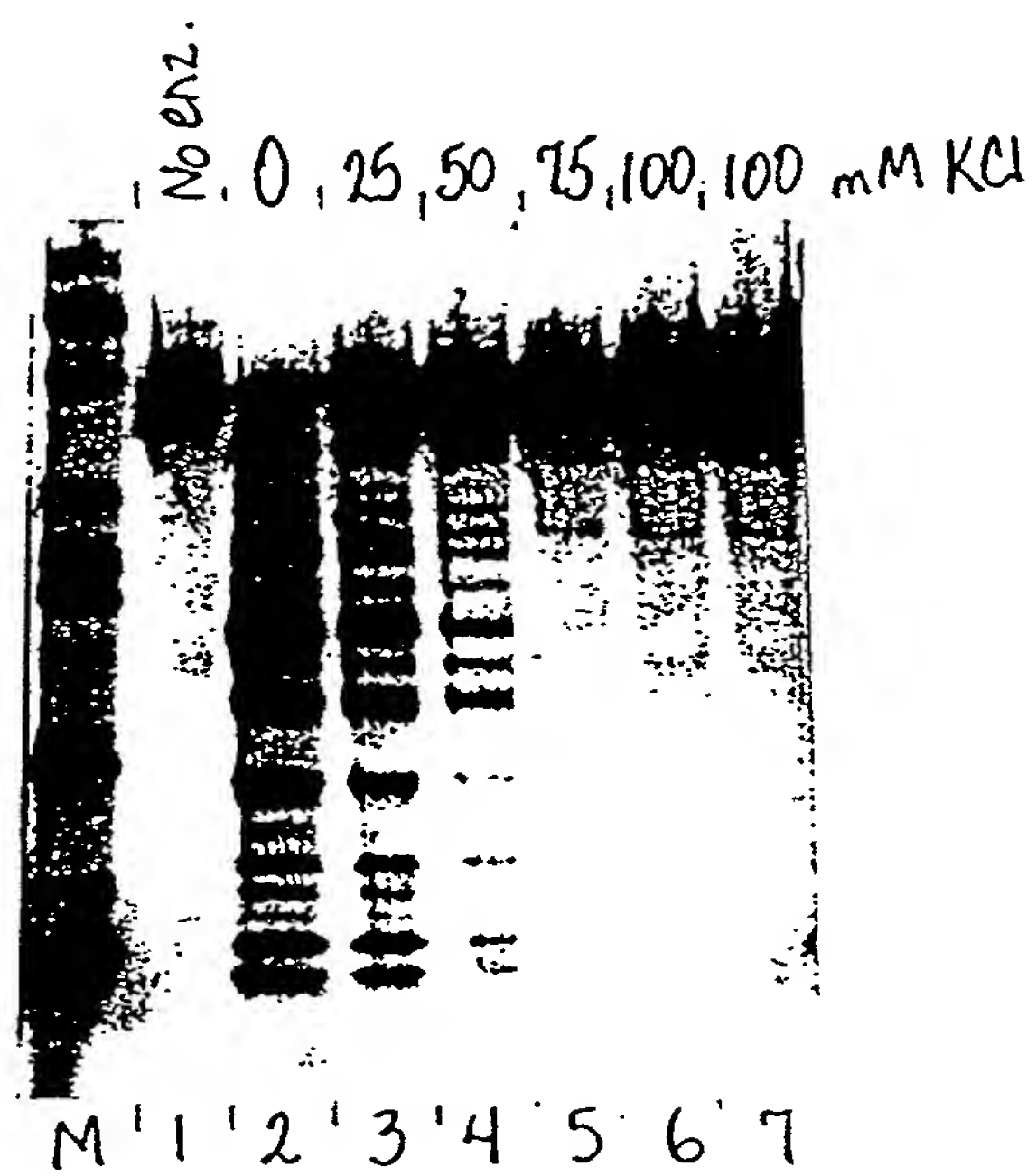


FIGURE 55

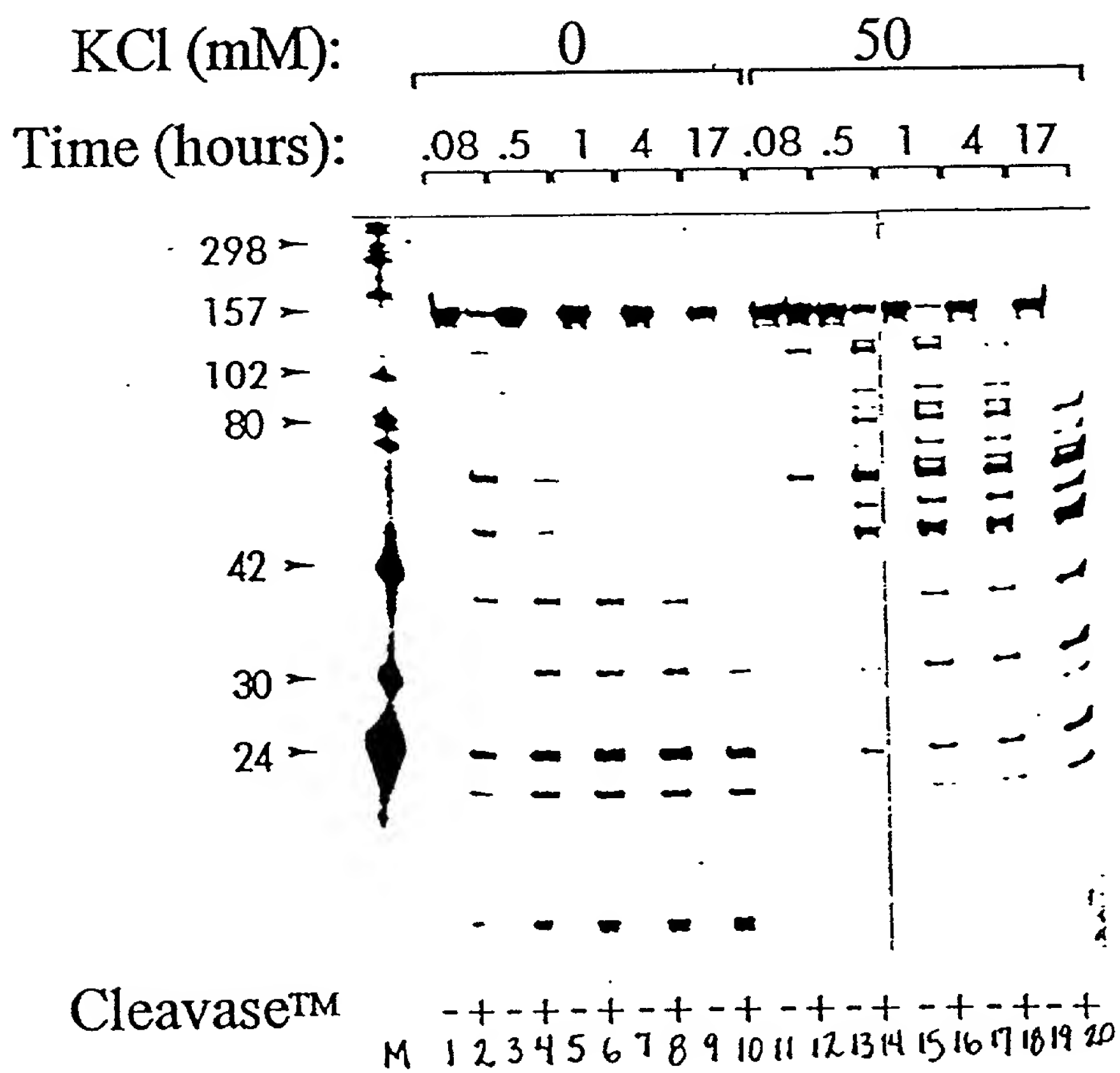


FIGURE 56

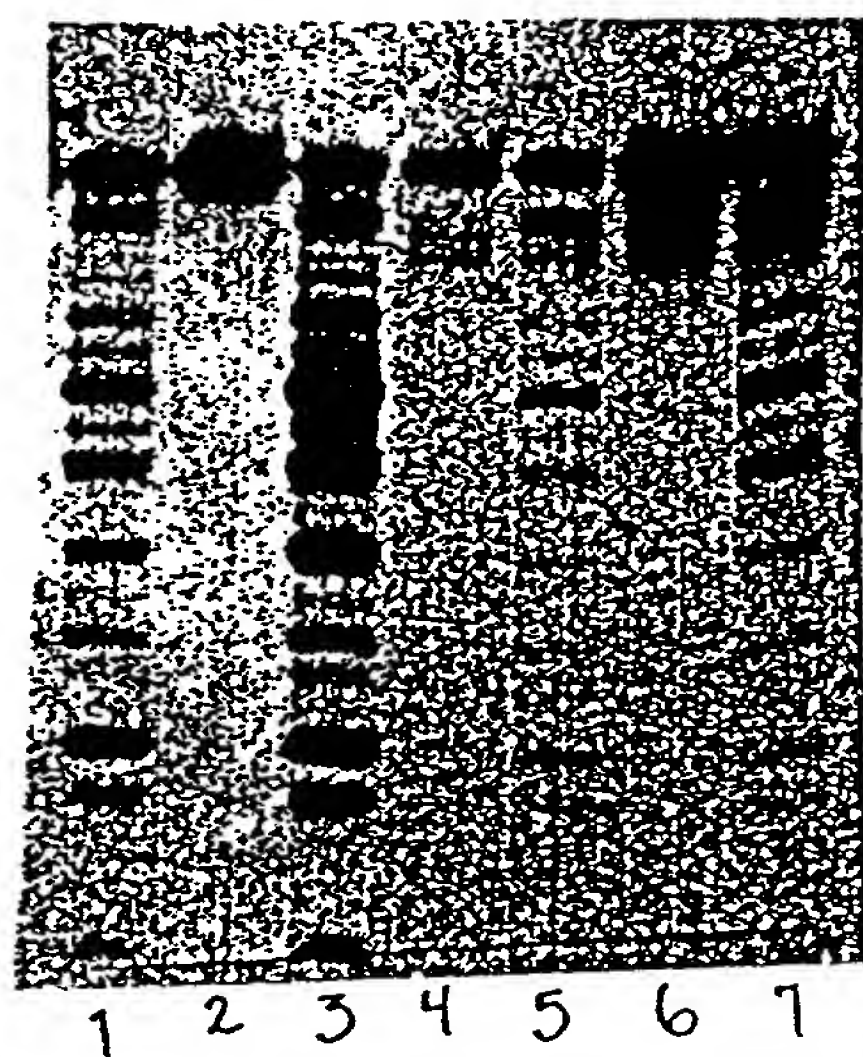


FIGURE 57

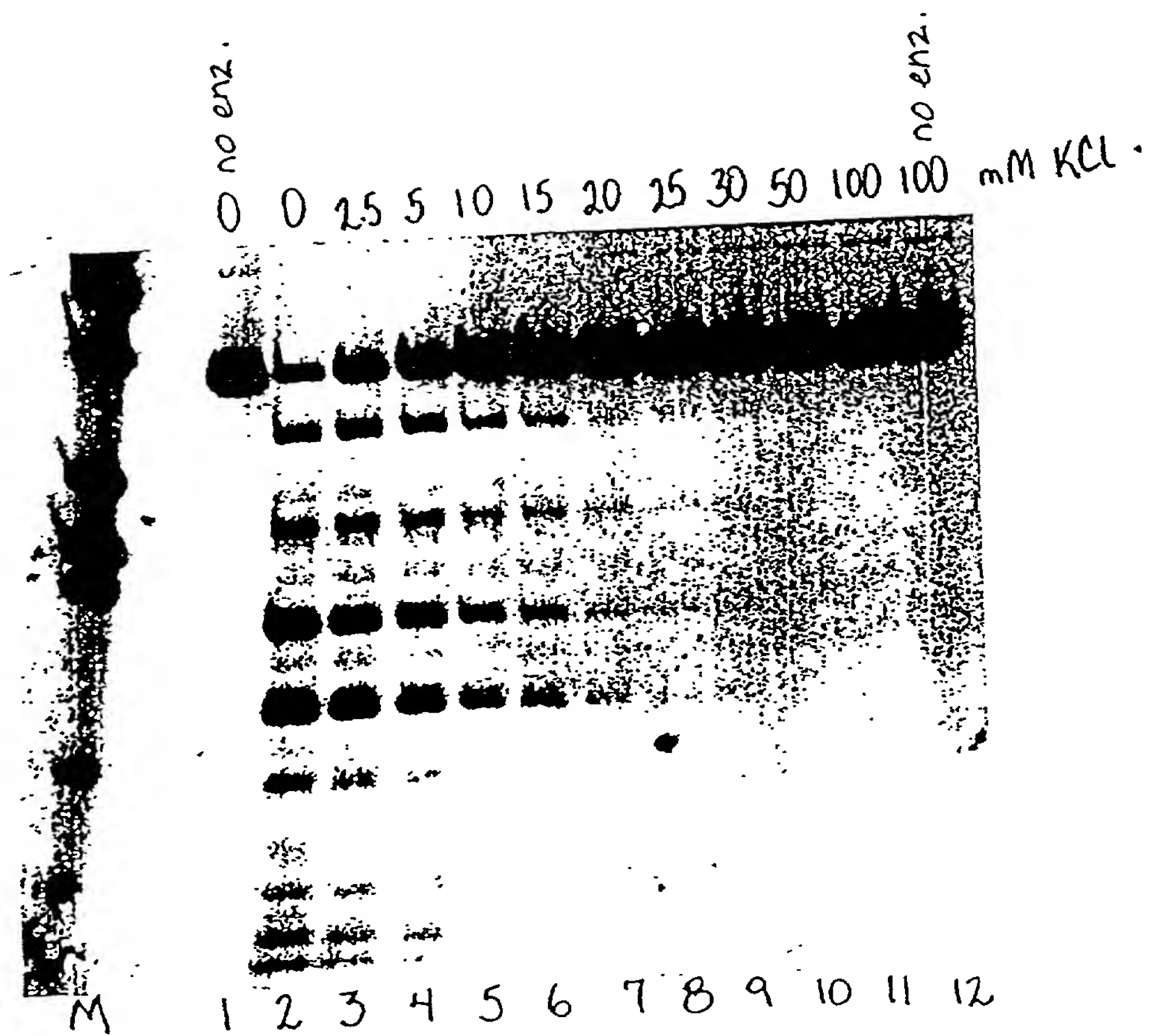


FIGURE 58

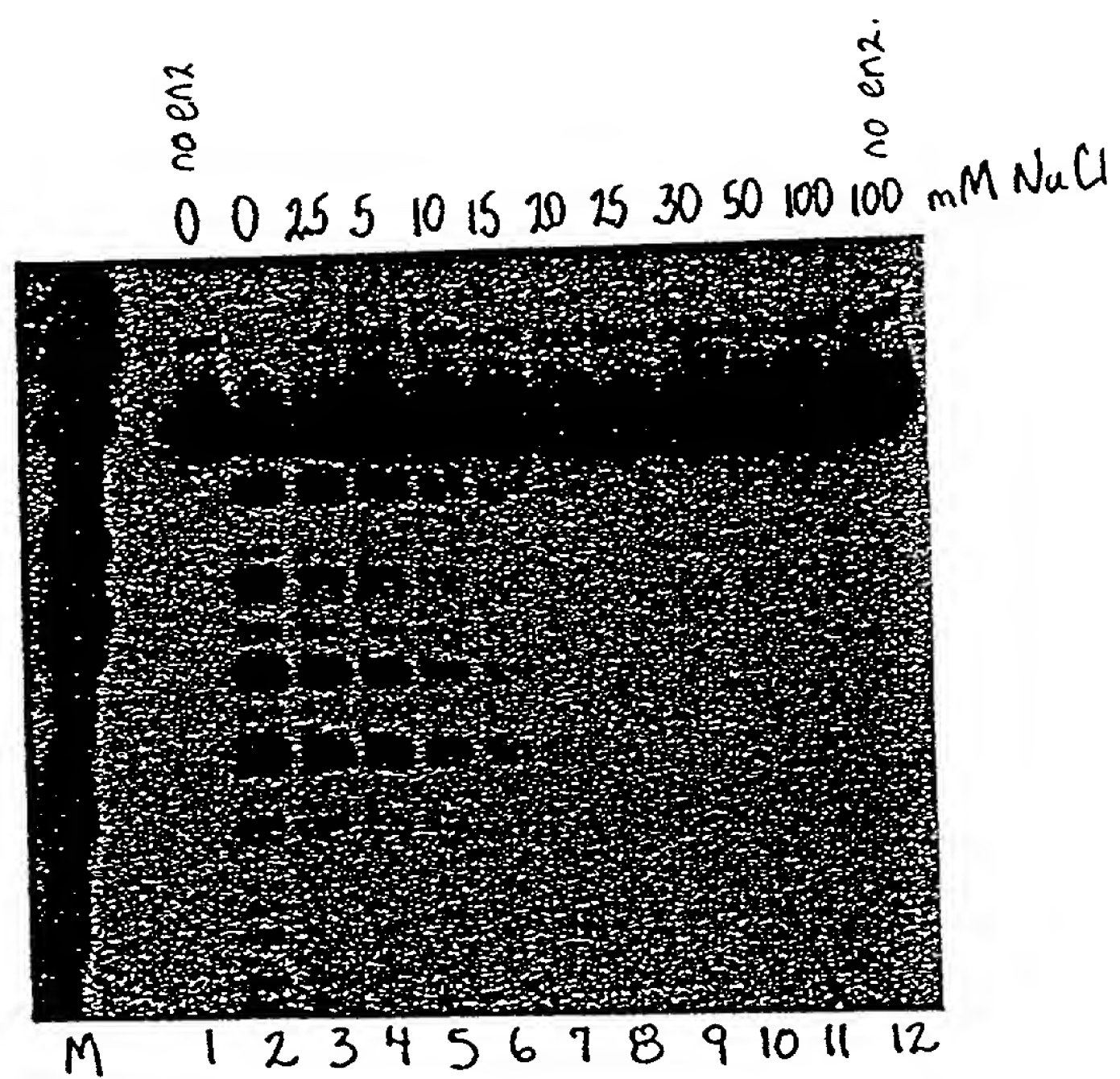


FIGURE 59

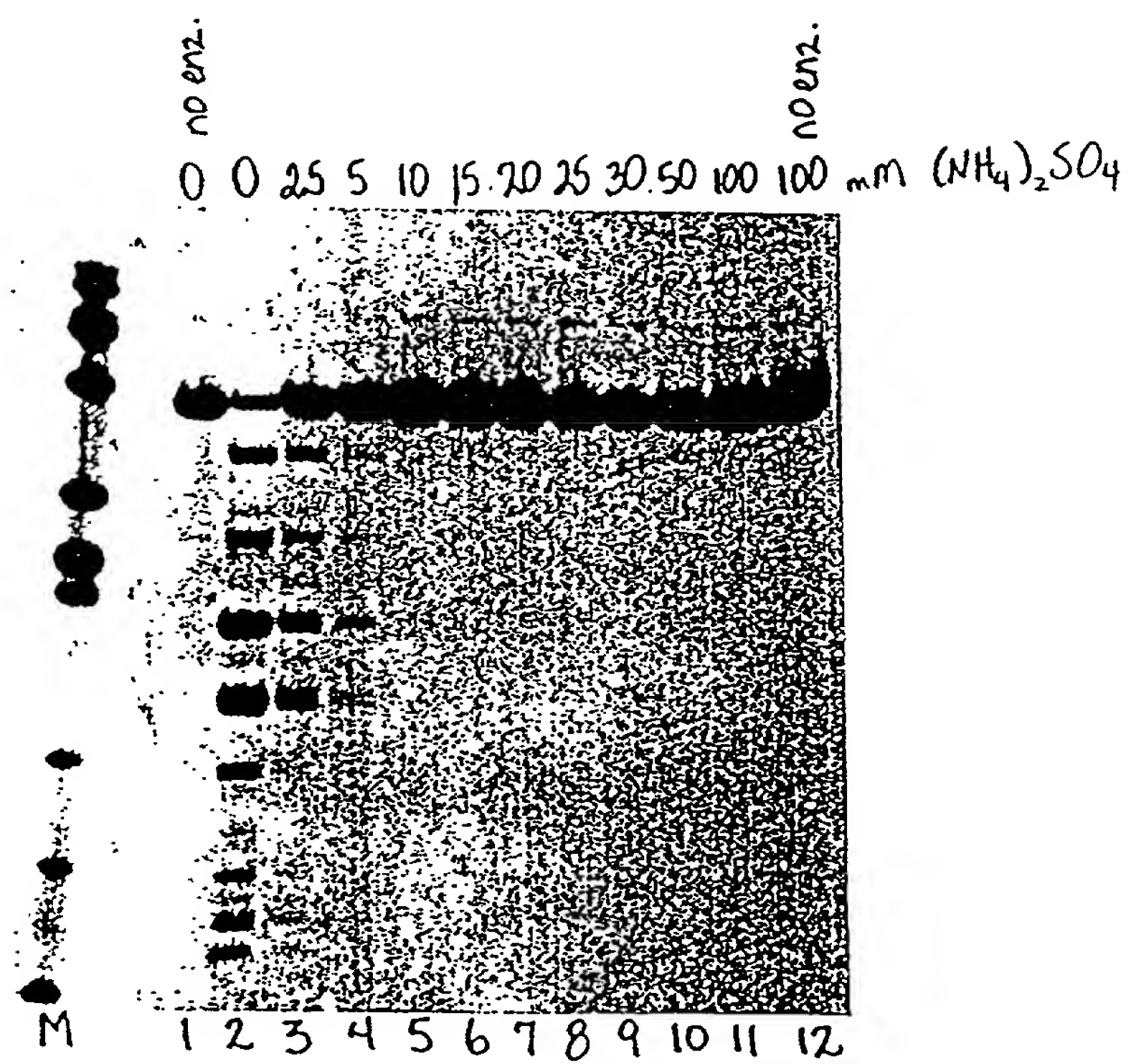


FIGURE 60

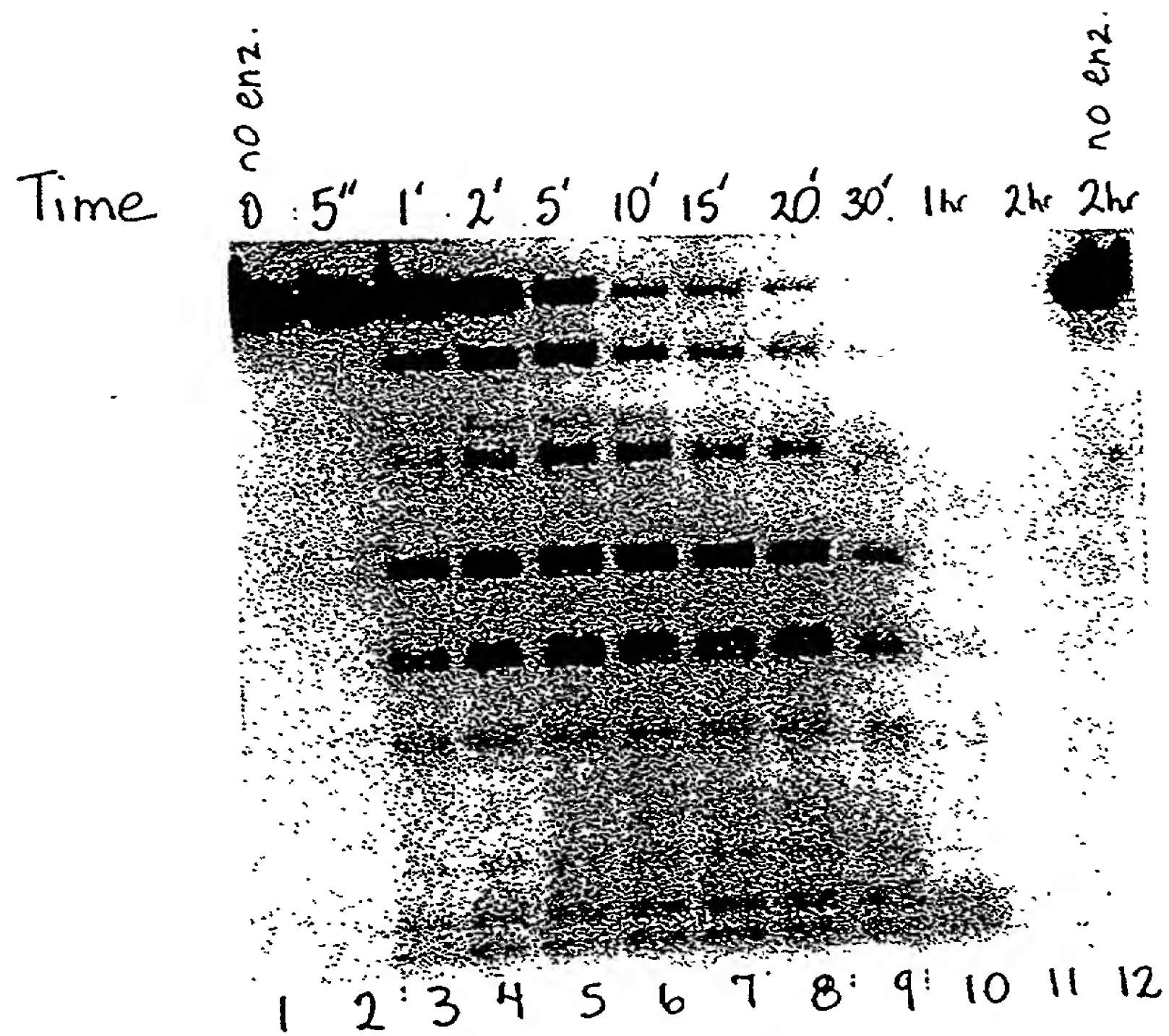


FIGURE 61

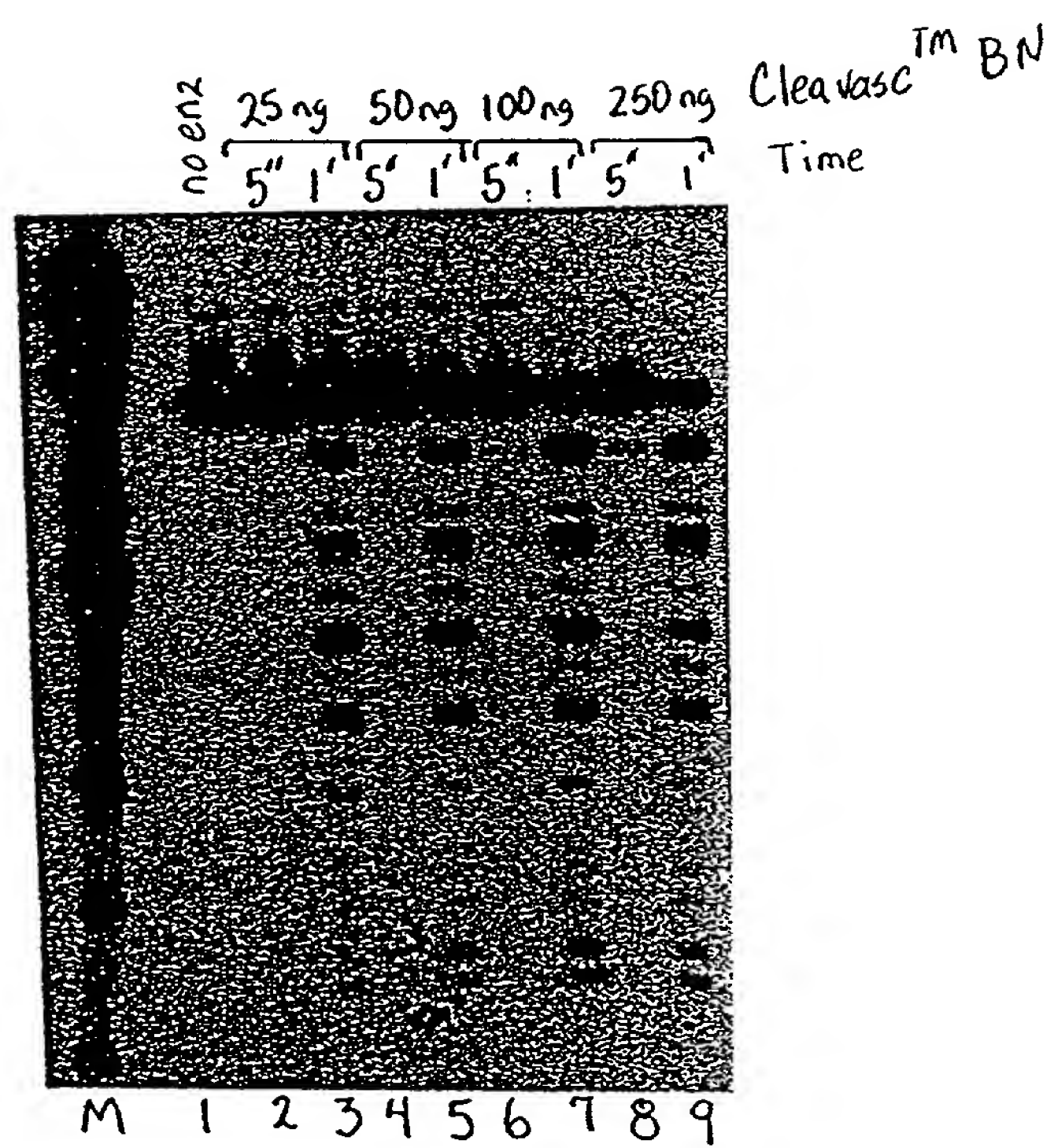


FIGURE 62

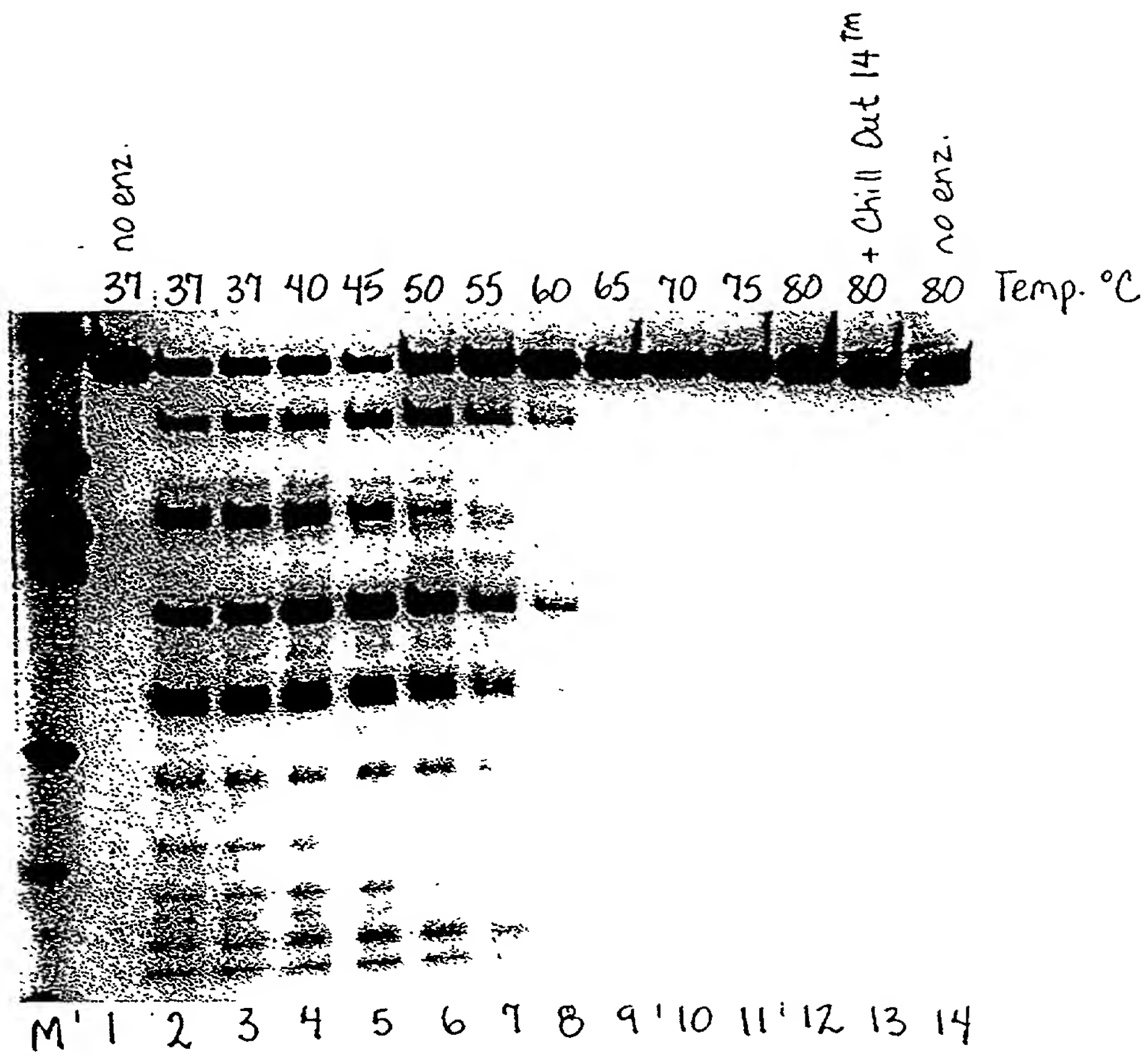


FIGURE 63

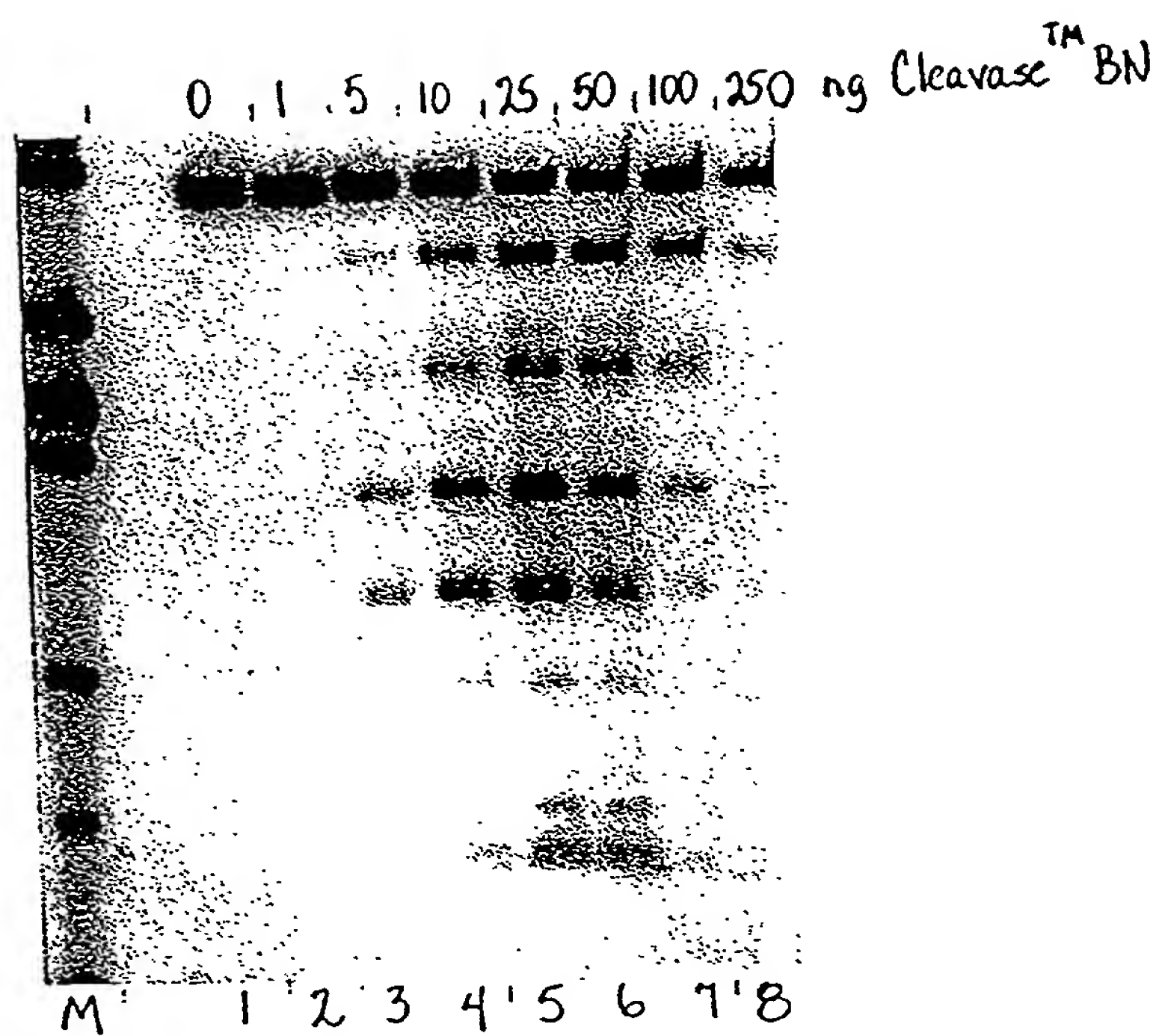
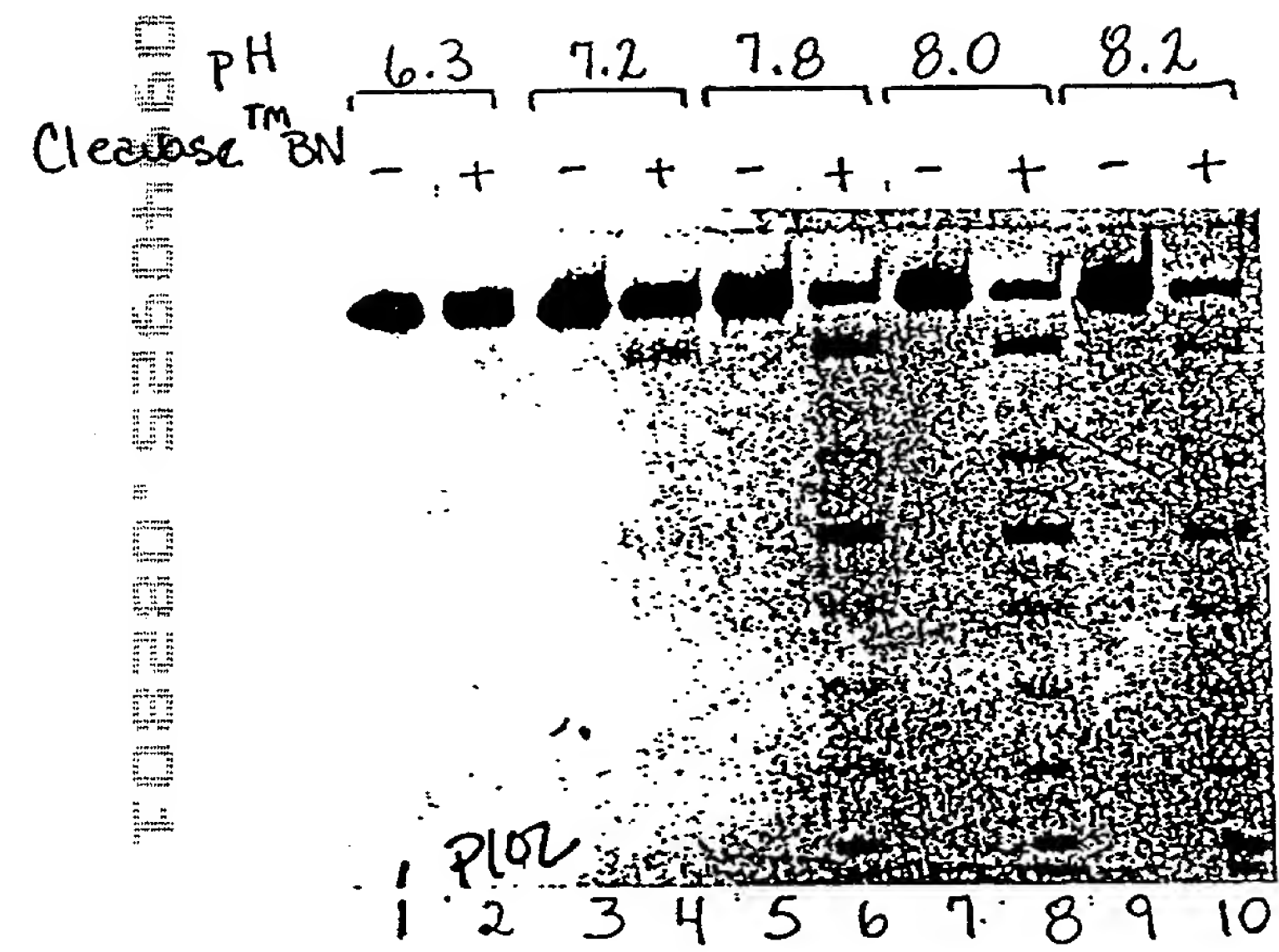


FIGURE 64

A



B

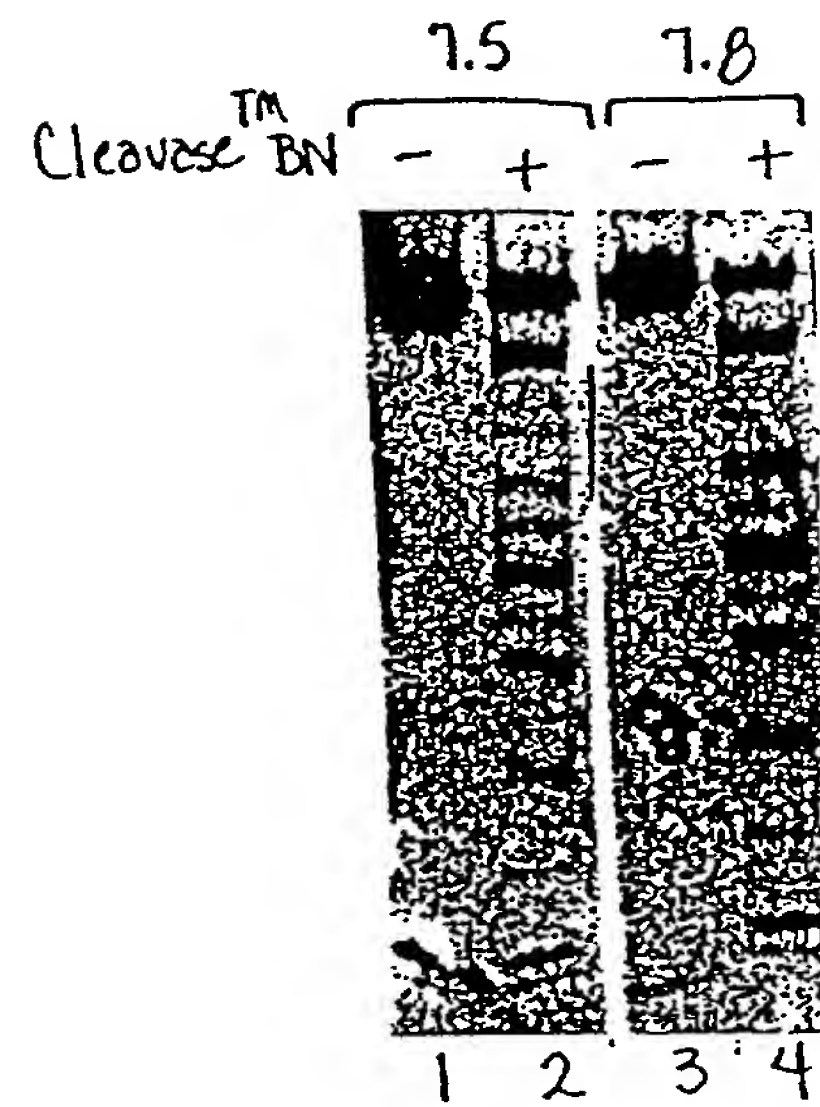
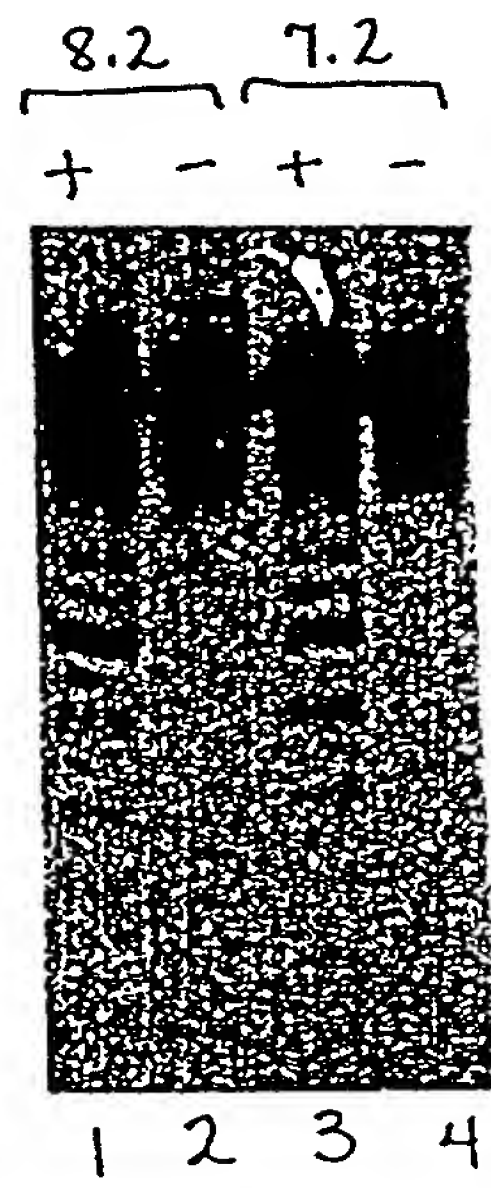


FIGURE 65

A



pH
Cleavase™ BN

B

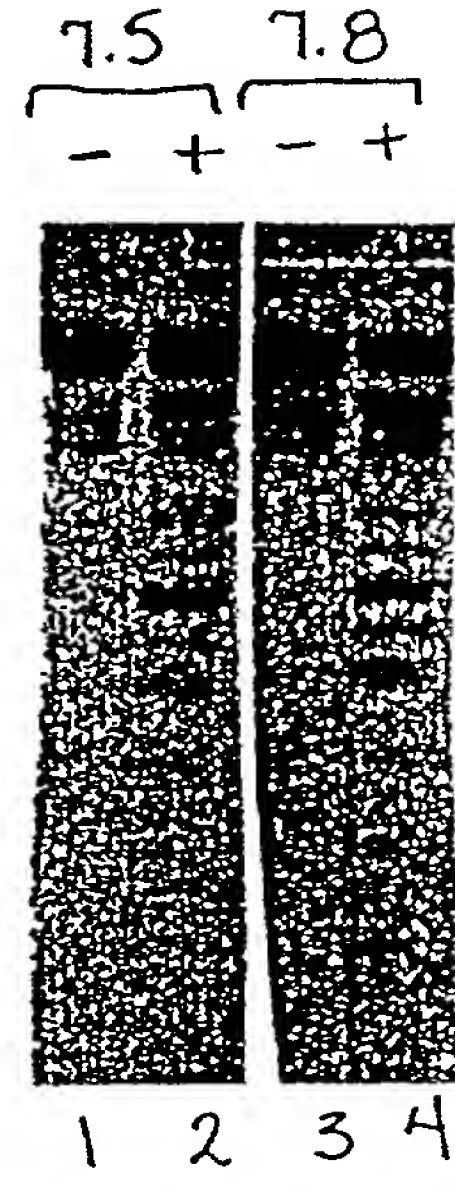


FIGURE 66

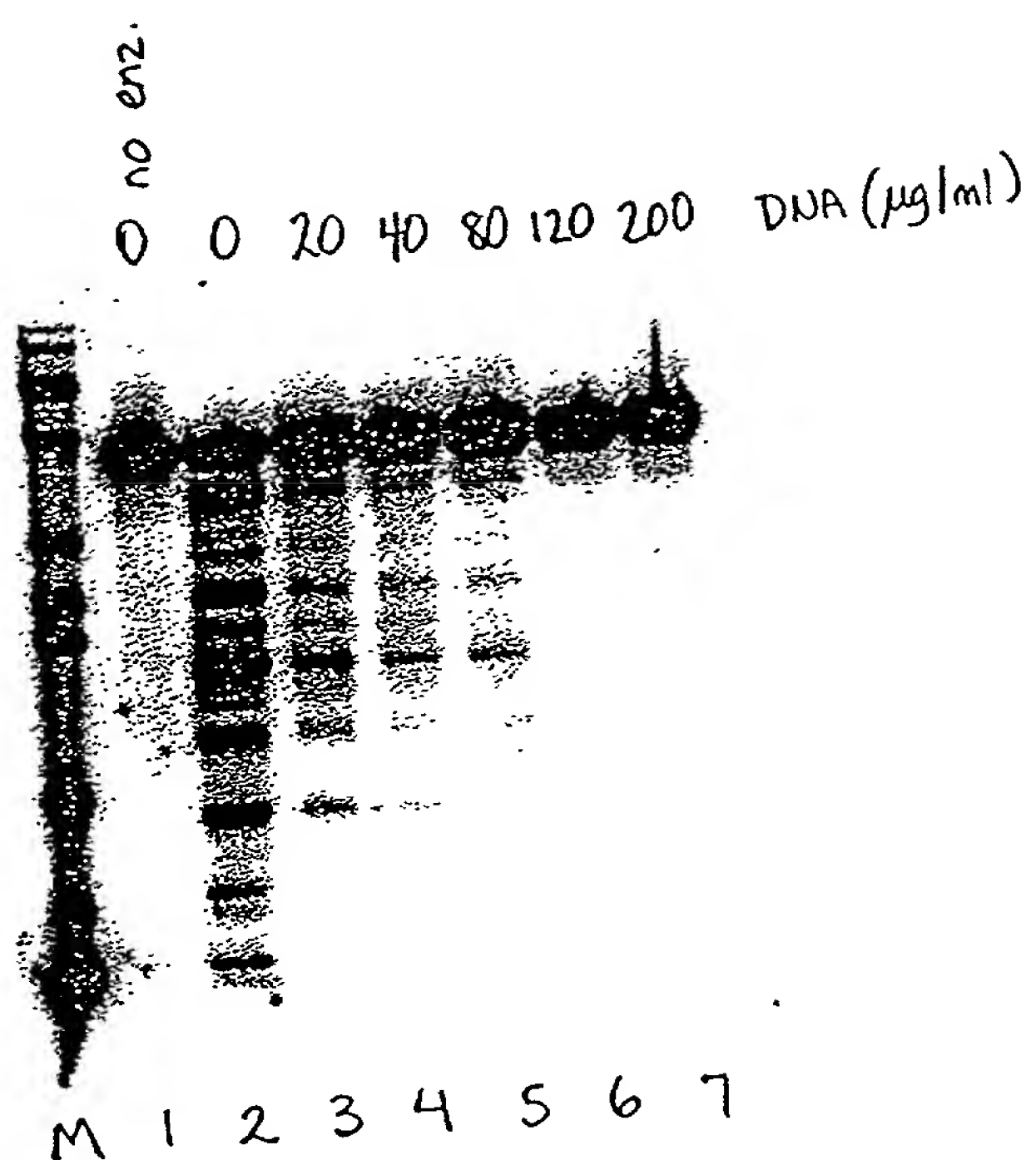


FIGURE 67

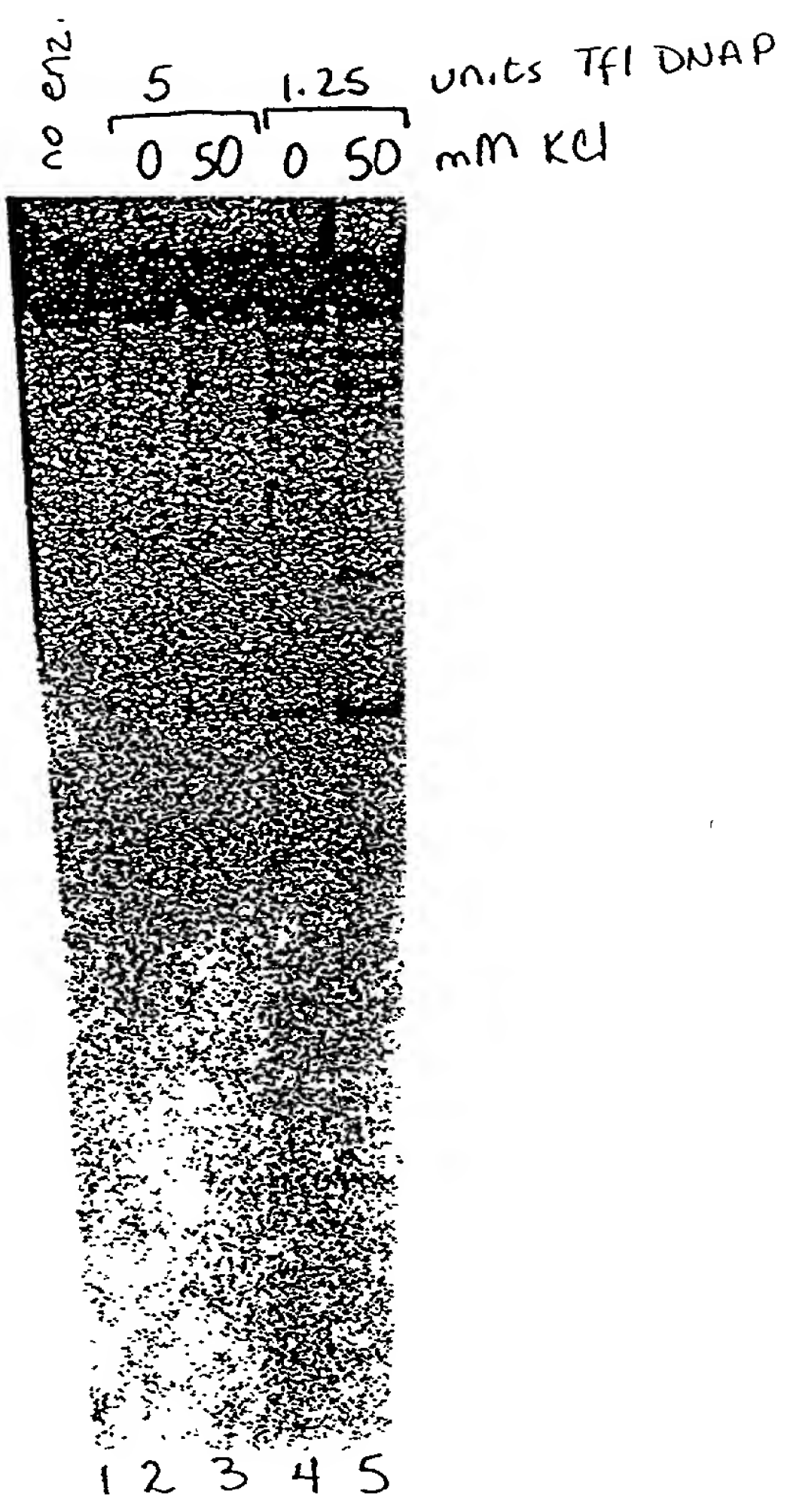


FIGURE 68

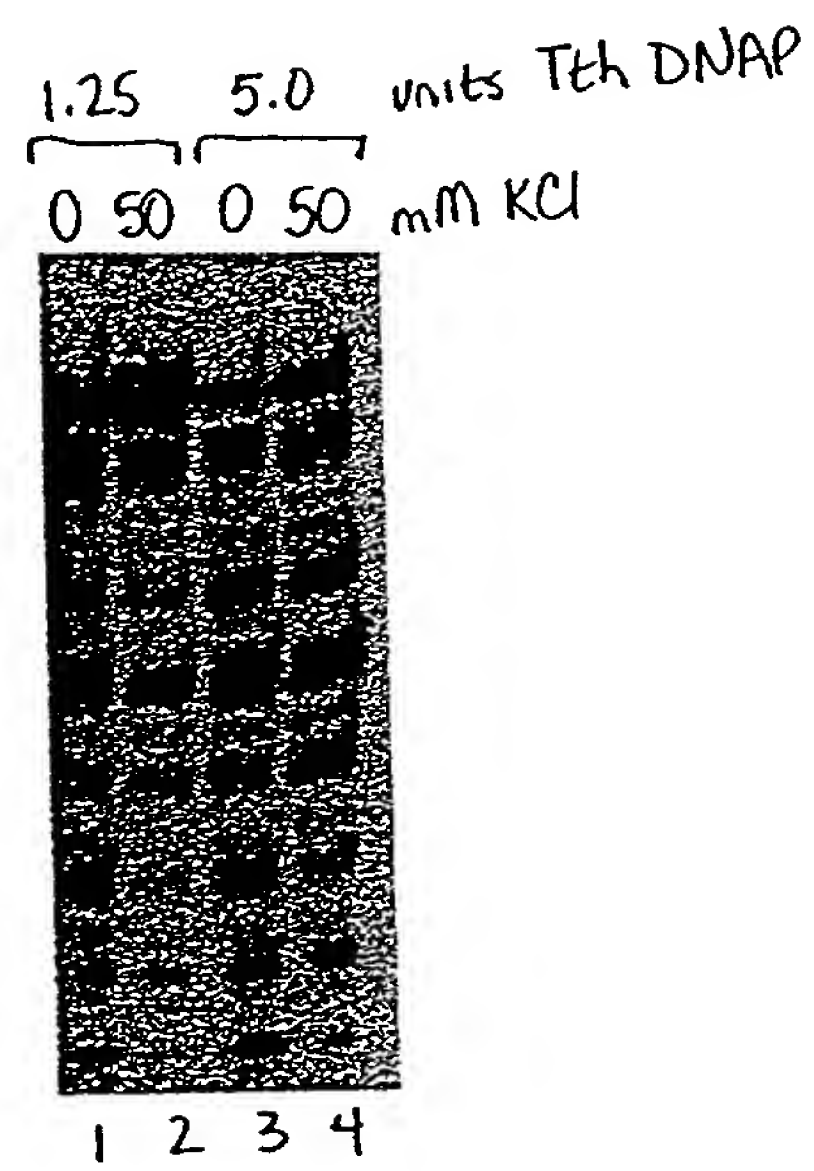


FIGURE 69

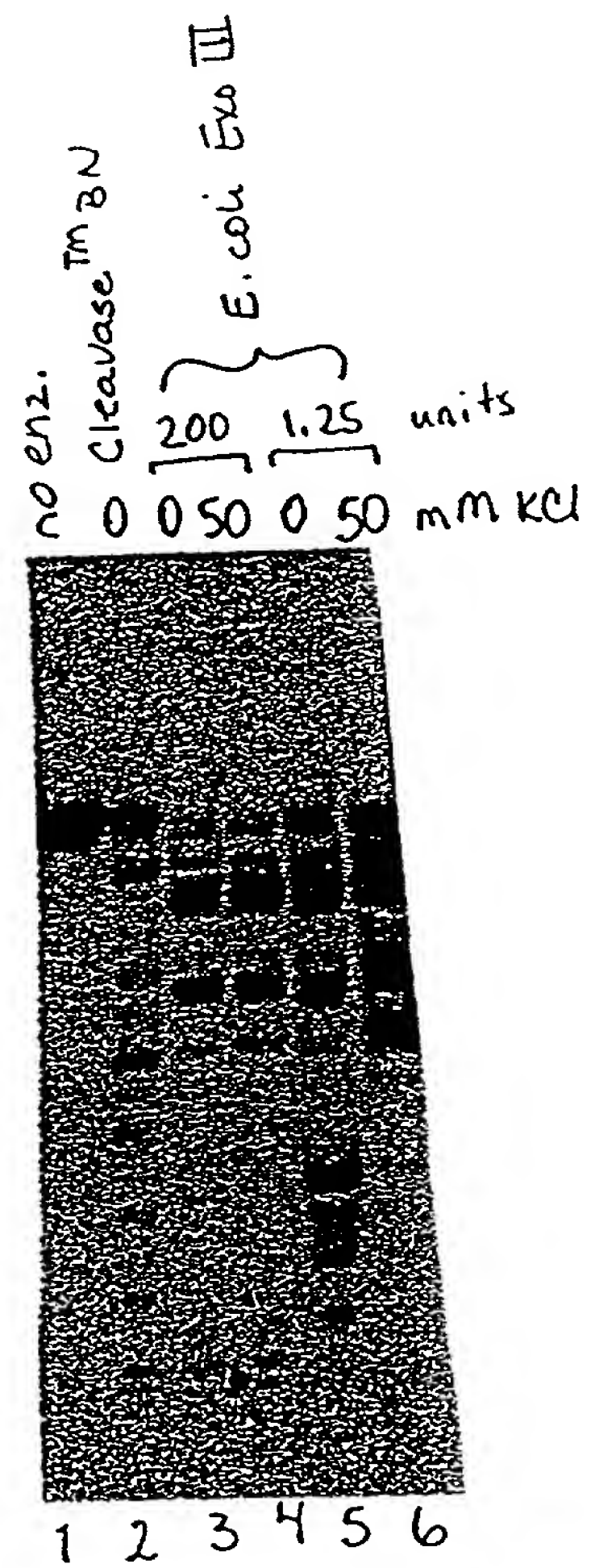


FIGURE 70

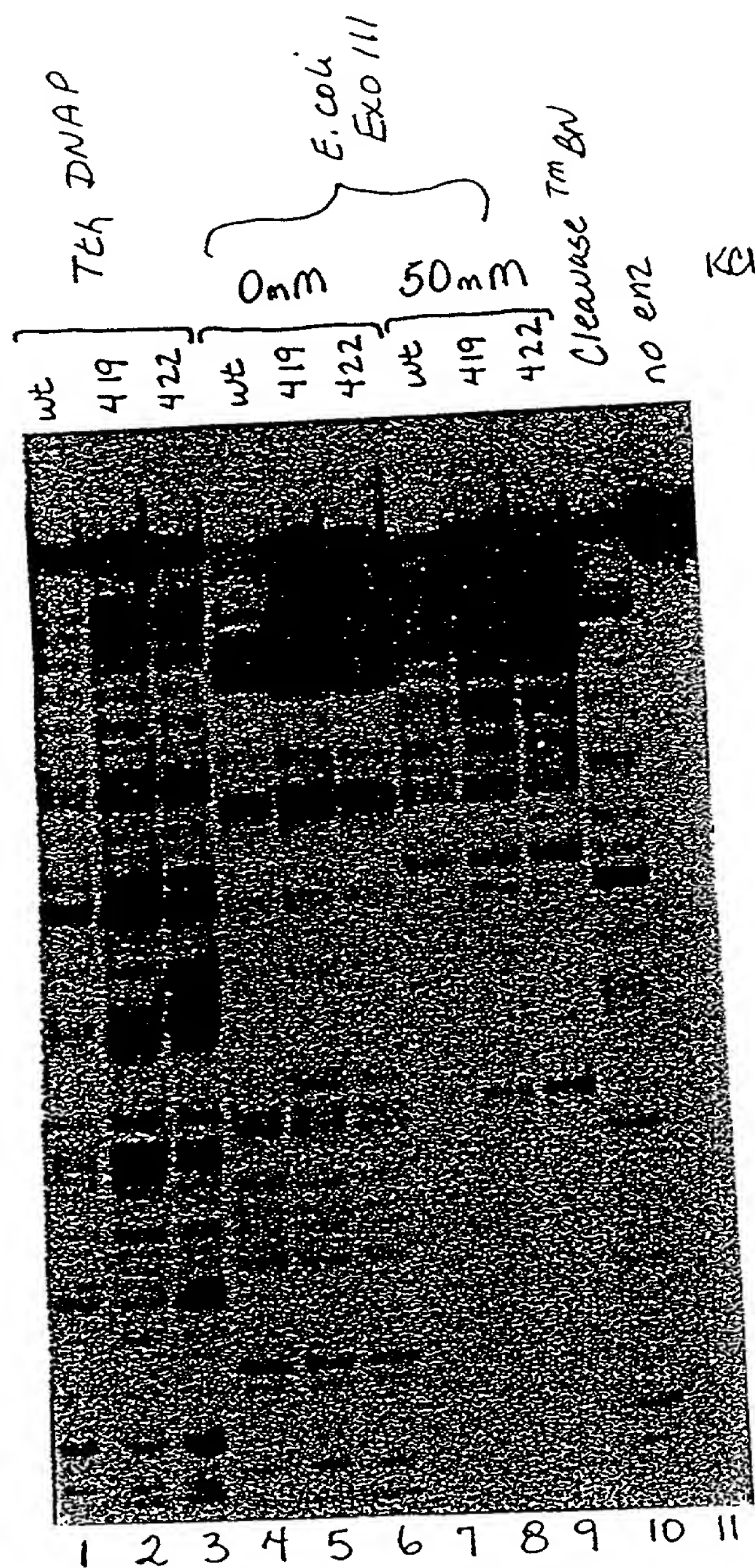


FIGURE 71

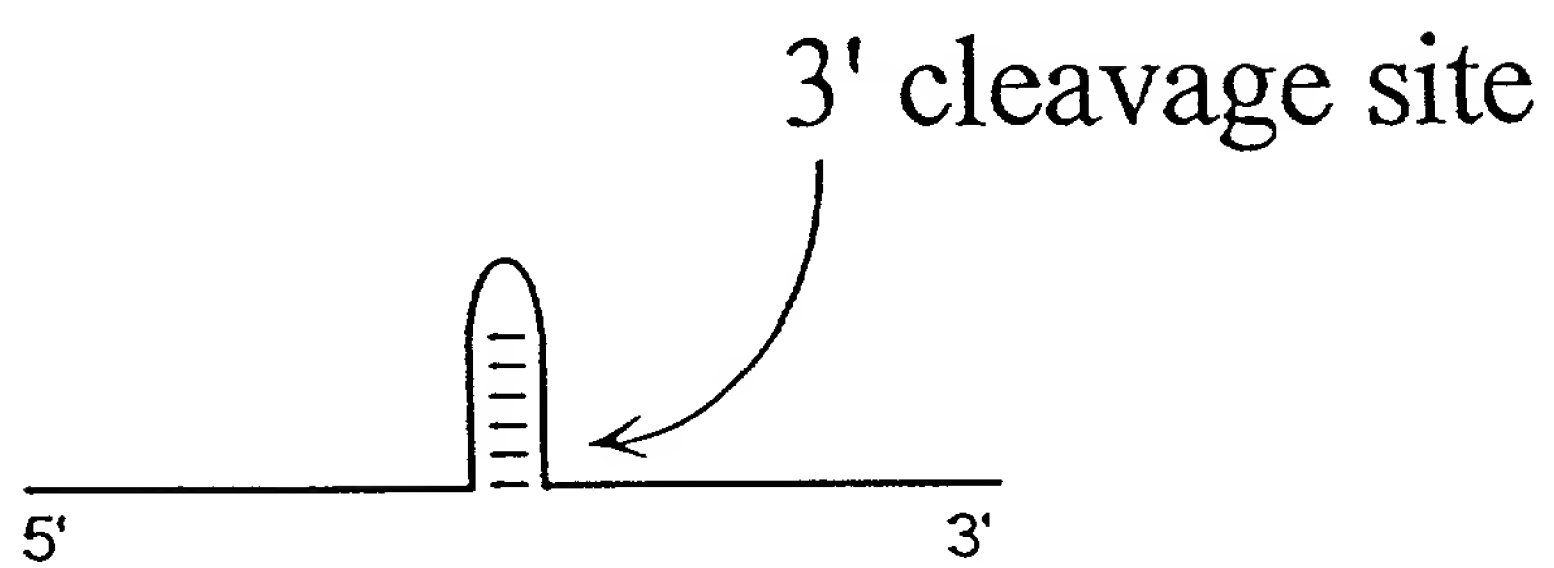
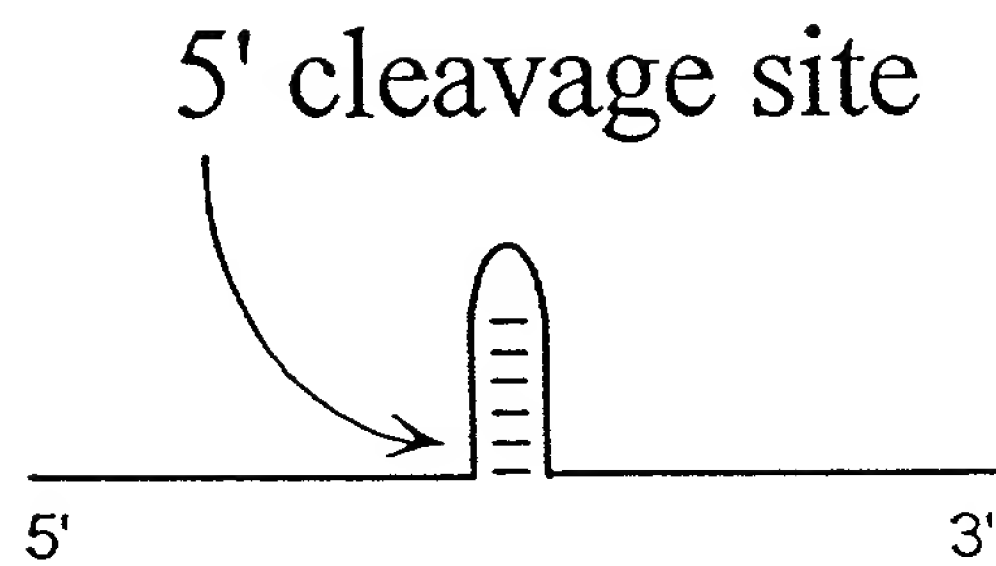


FIGURE 72

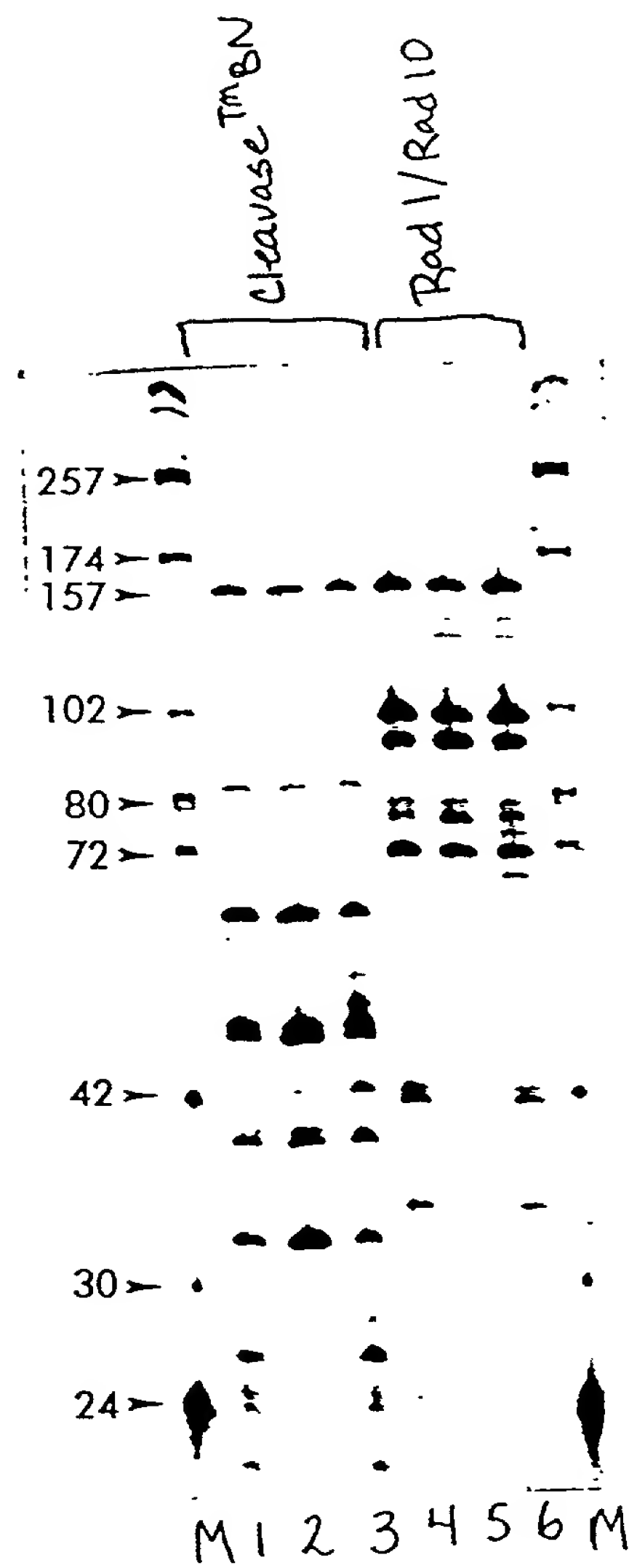


FIGURE 73

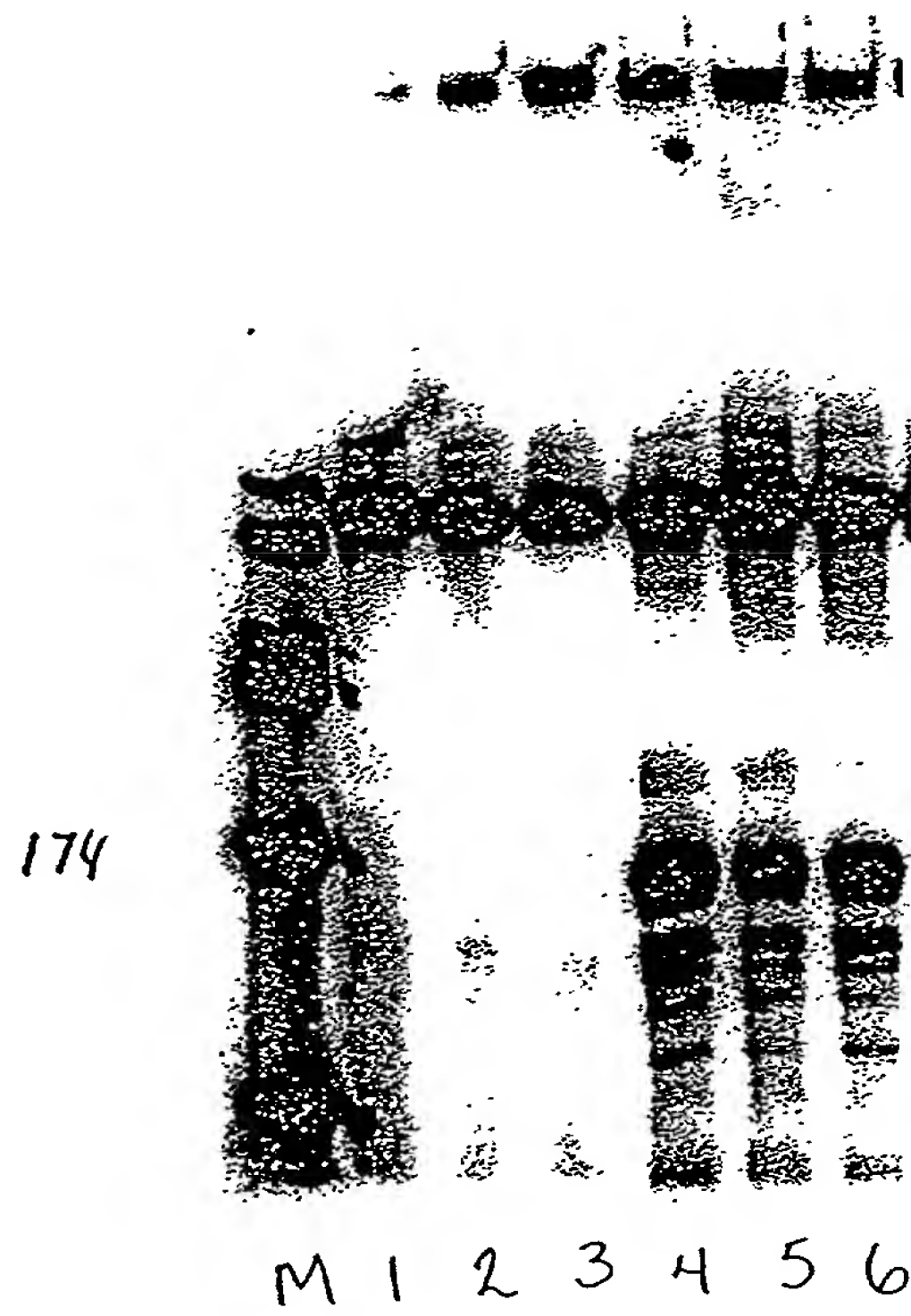


FIGURE 74

A

B

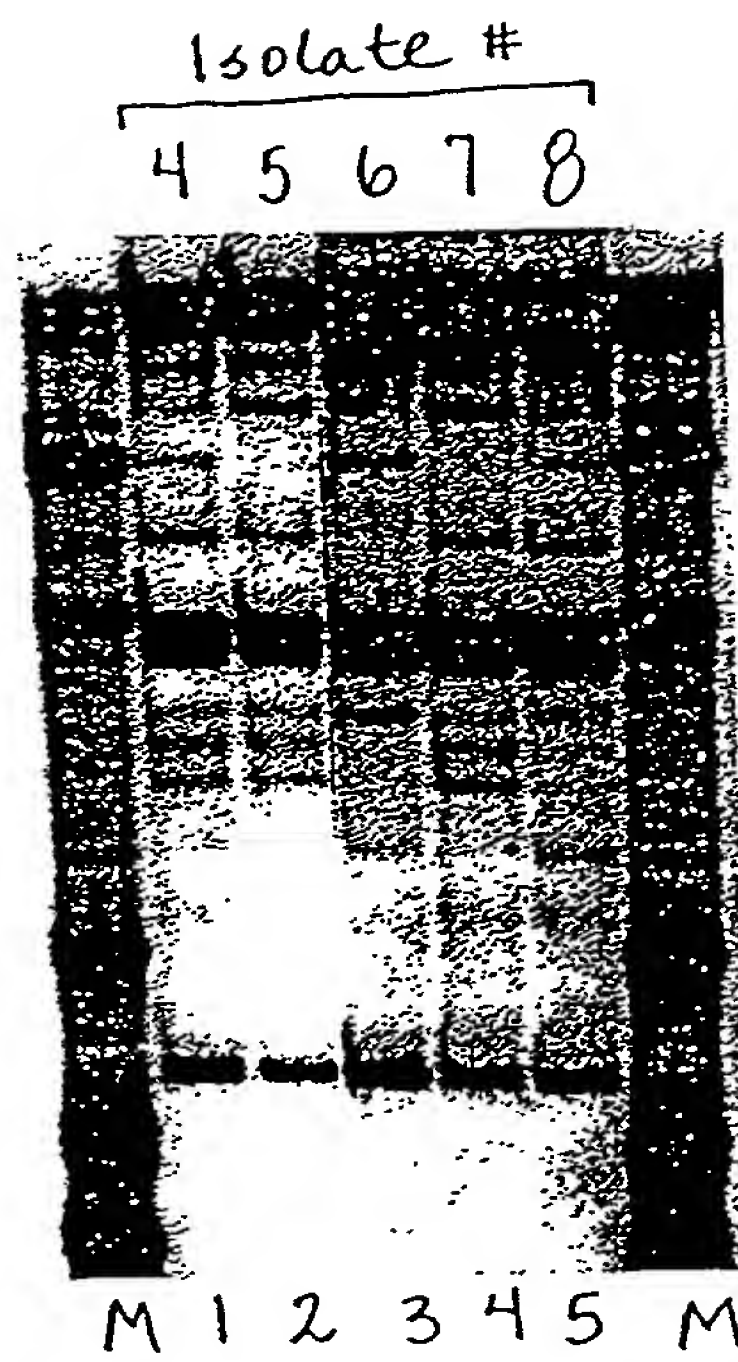
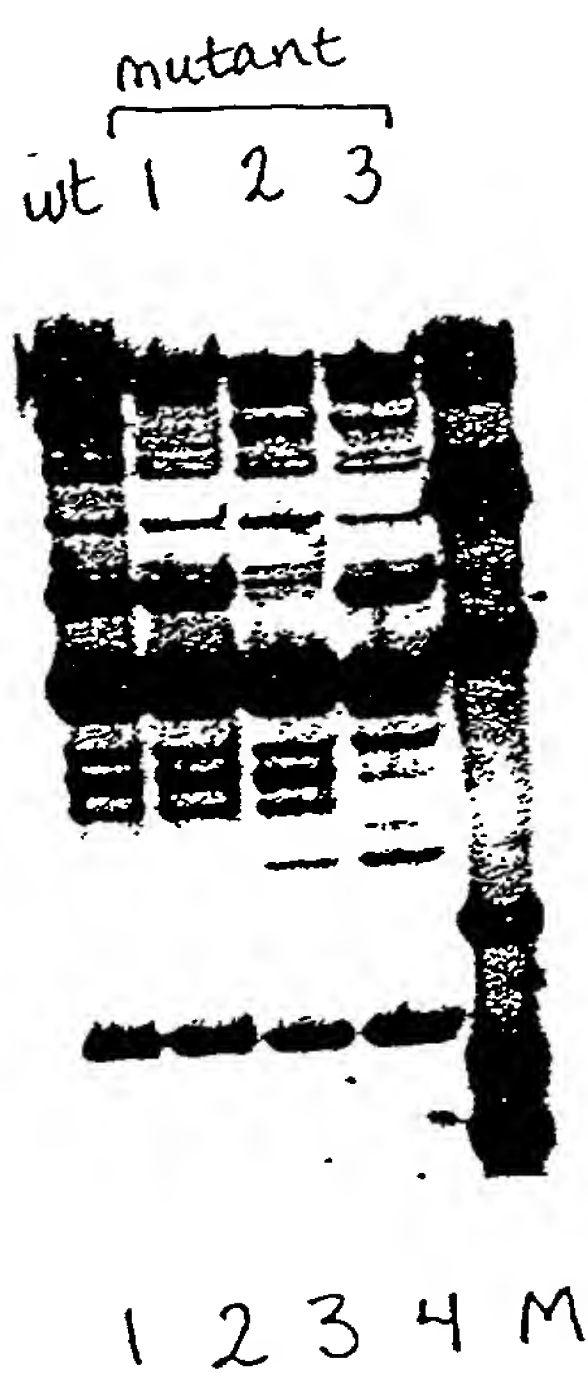


FIGURE 75

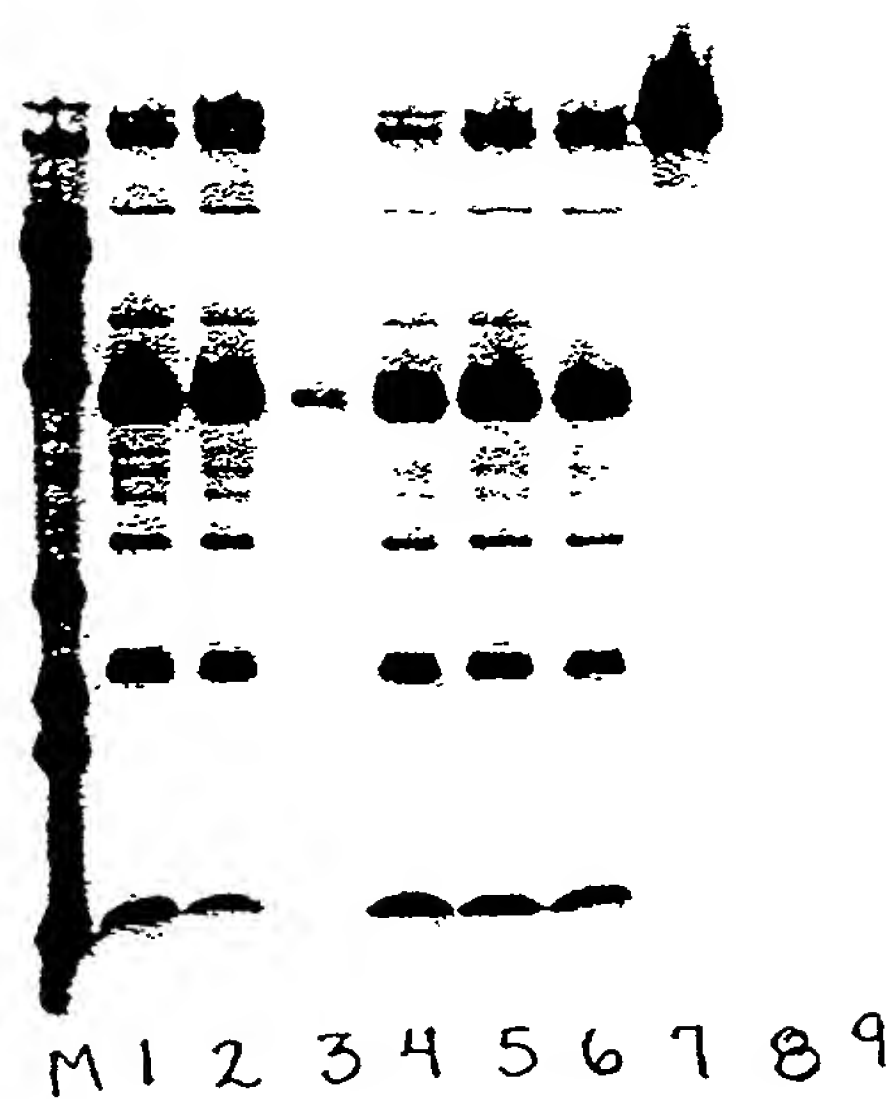


FIGURE 76

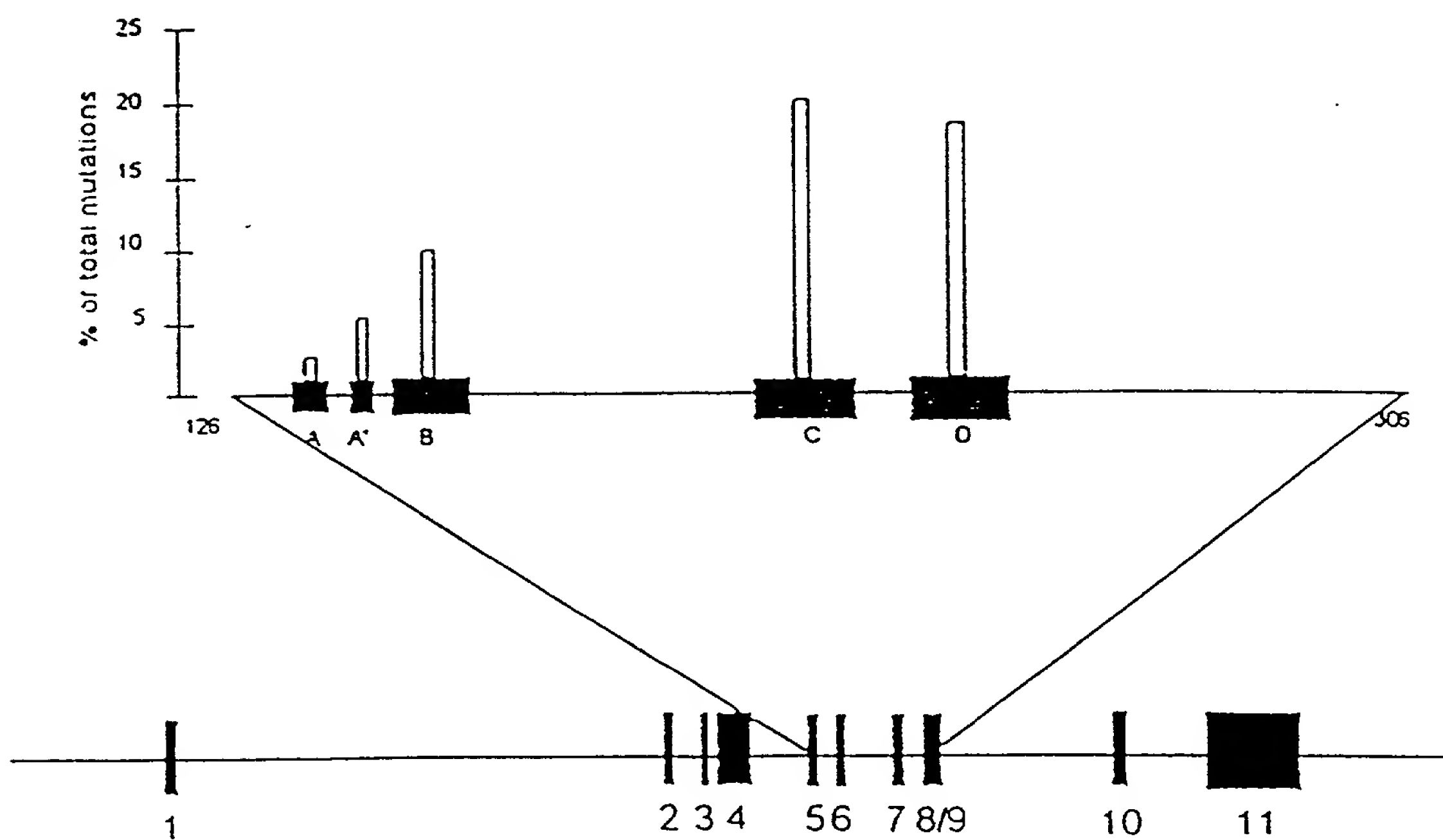
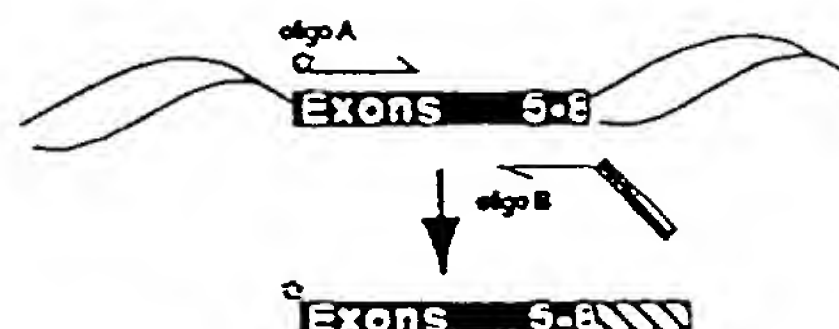


FIGURE 77

PCR 1 Generate Fragment Containing Mutation

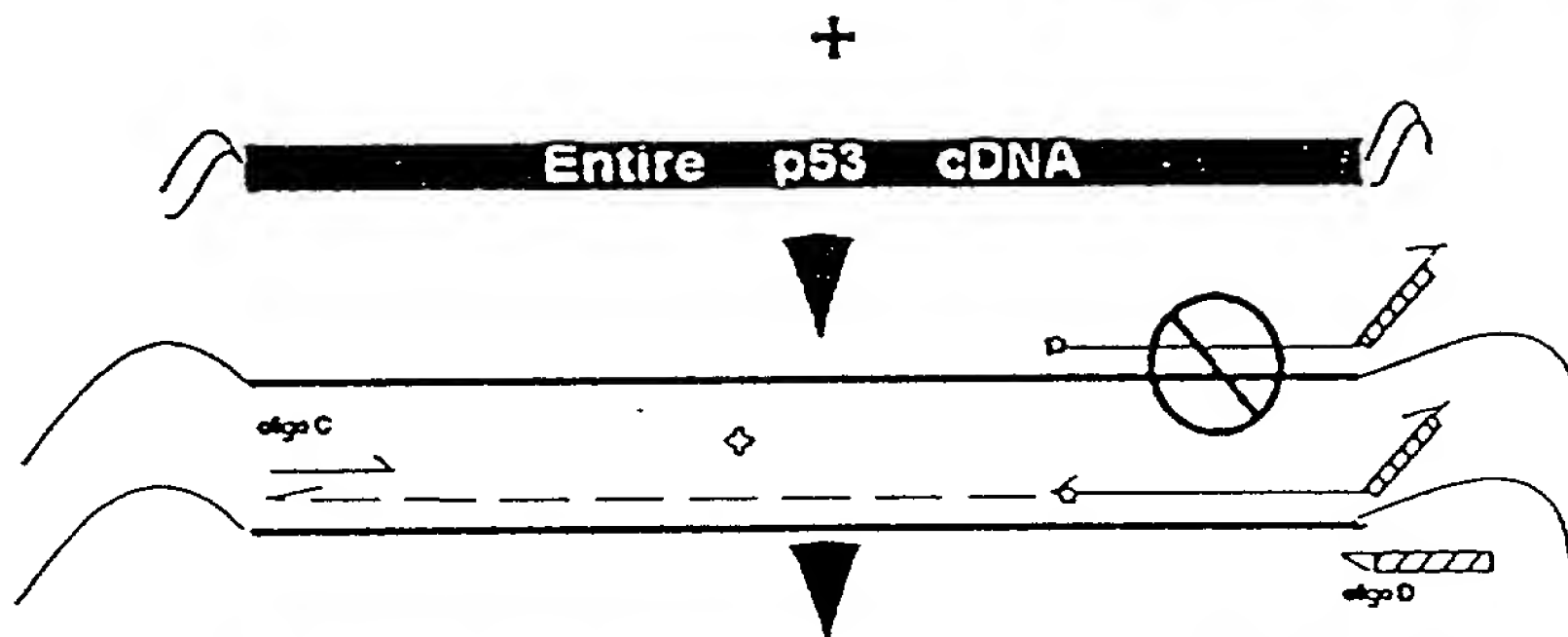


Add Amplified Fragment to PCR 2

PCR 2



Denature and Amplify



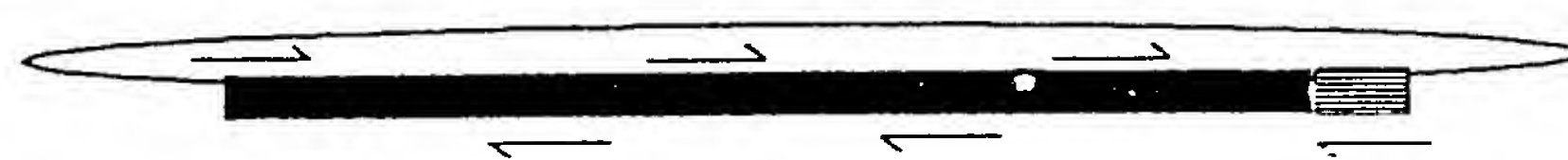
Insert Mutant into Fragment by PCR



Digest and Clone into Vector



Sequence and Archive



PCR Amplify Exons 5-8



CFLP Analysis of Exons 5-8

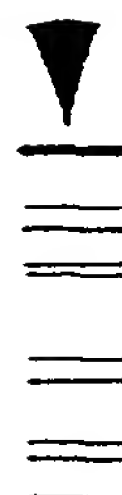
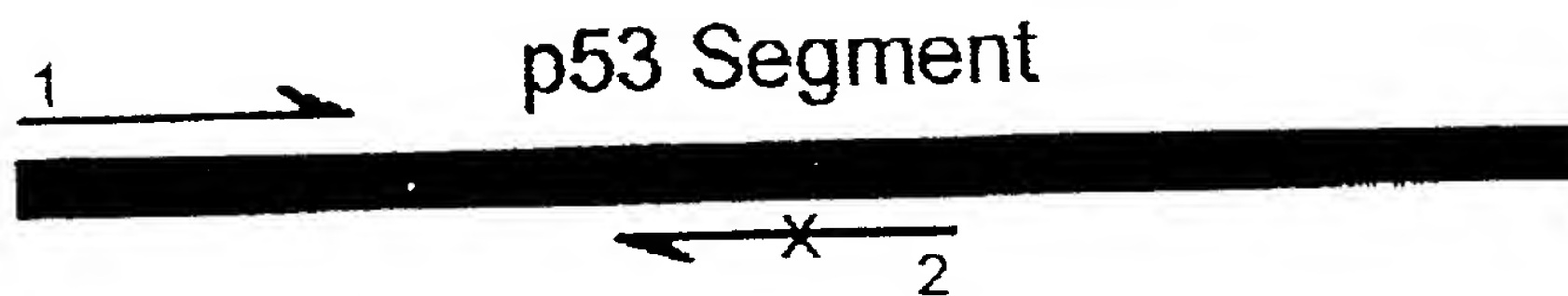
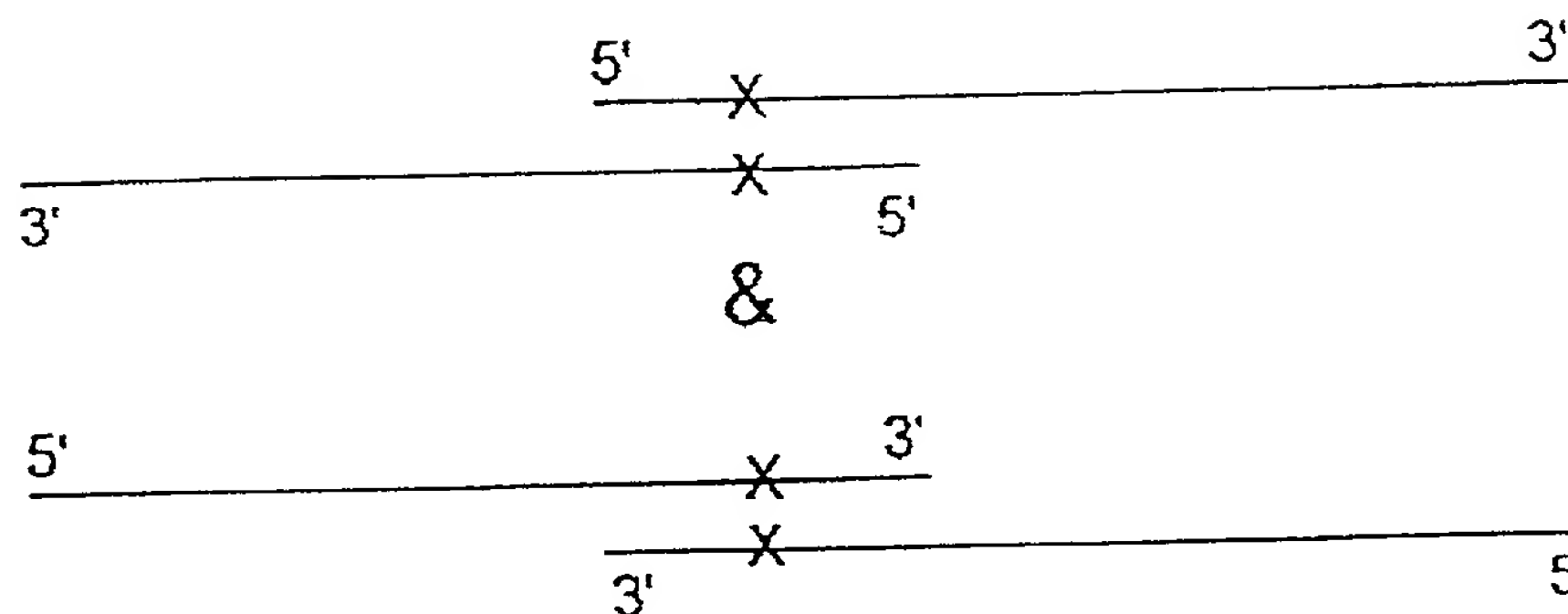
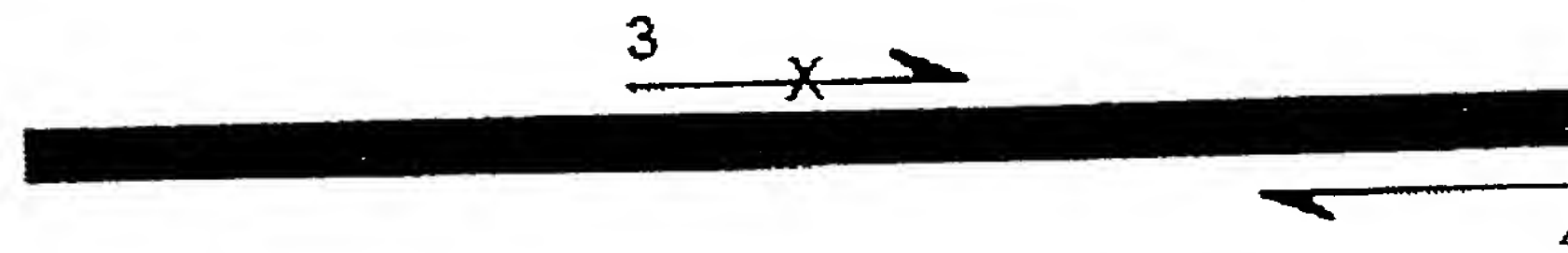


FIGURE 78

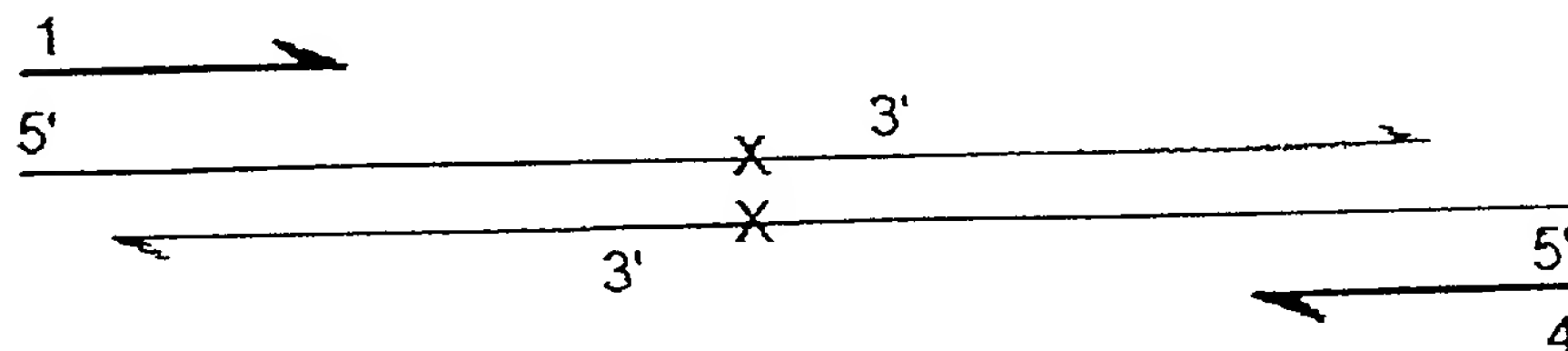
"upstream PCR"



"downstream PCR"



"Recombinant PCR"



Recombinant p53 segment



FIGURE 79

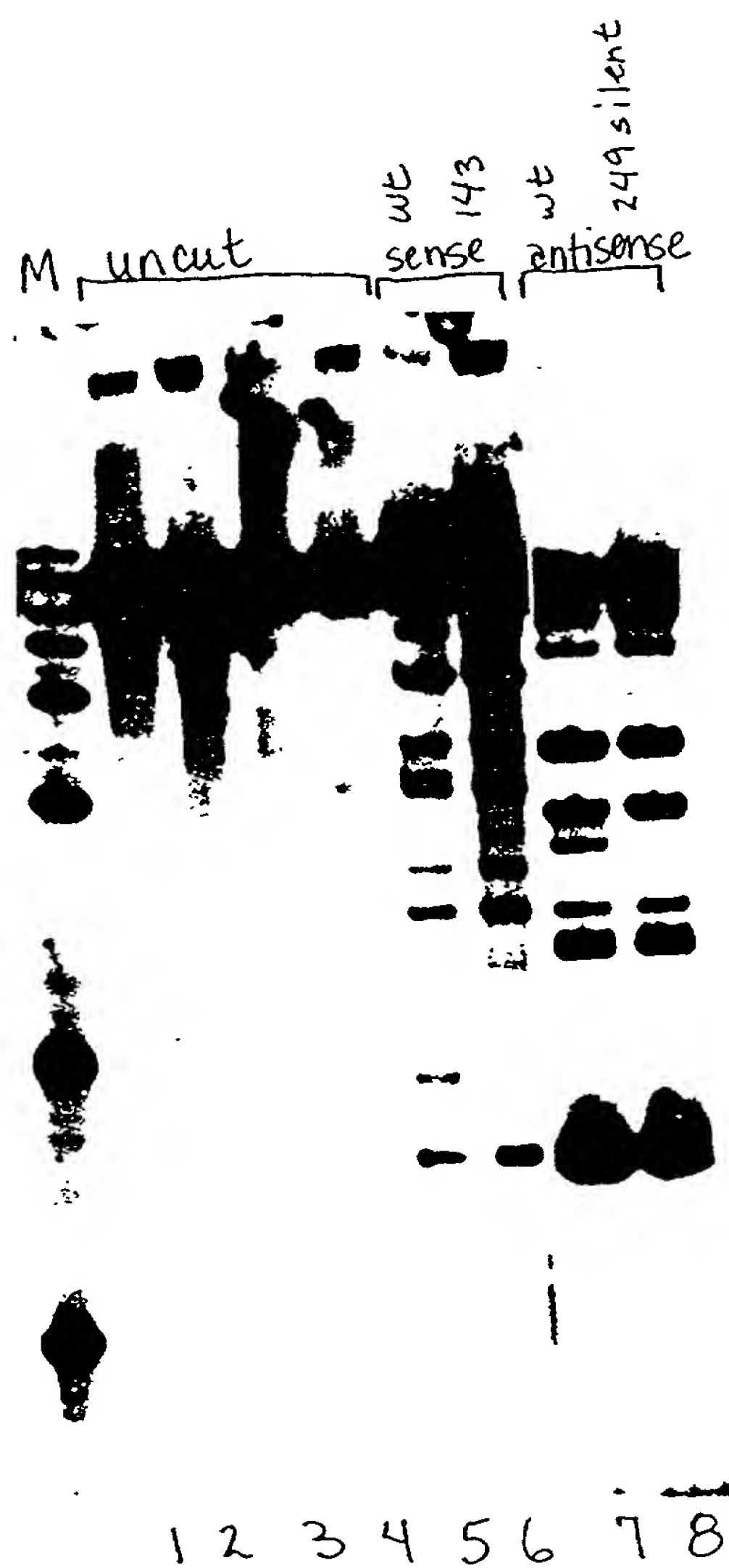


FIGURE 80

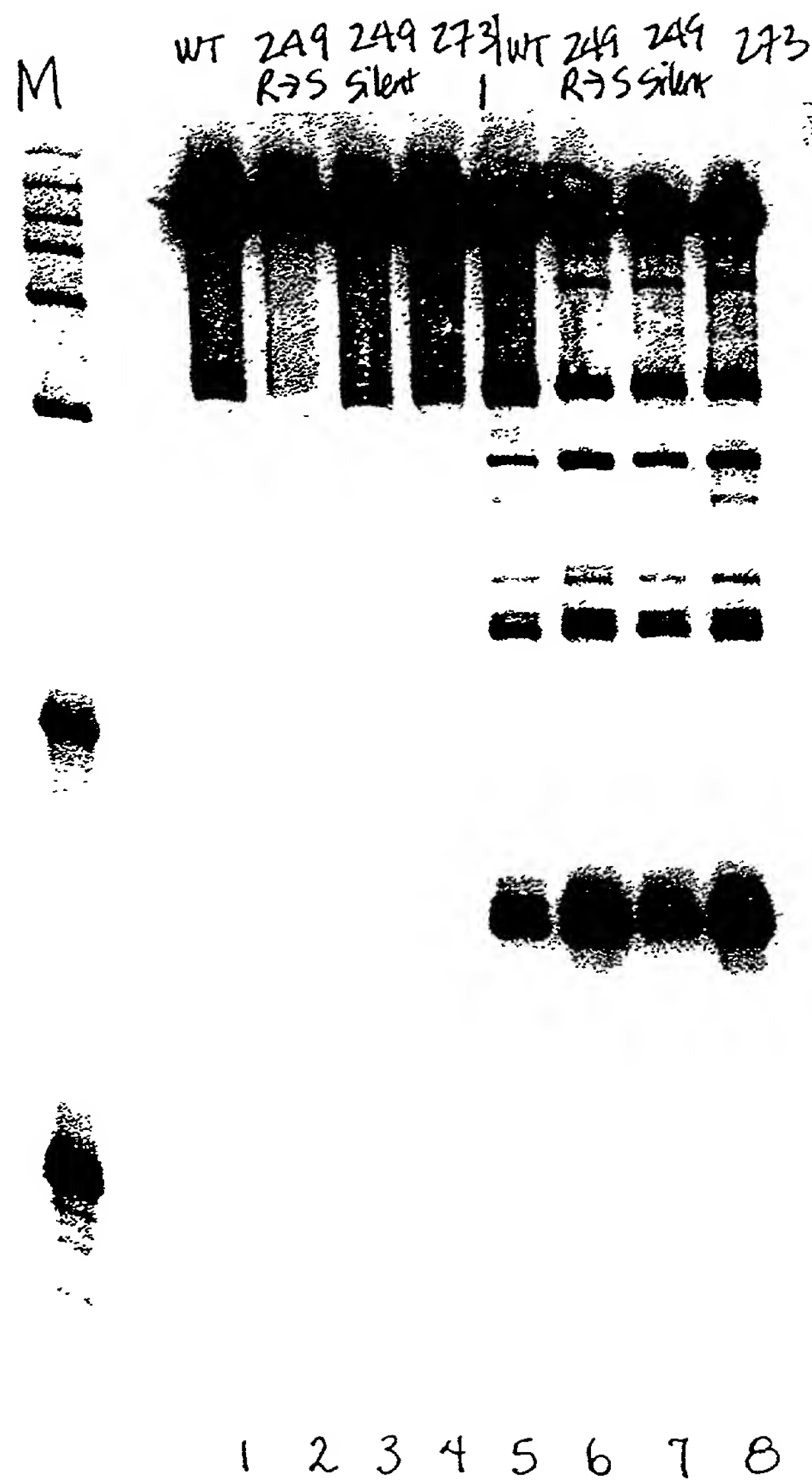


FIGURE 81

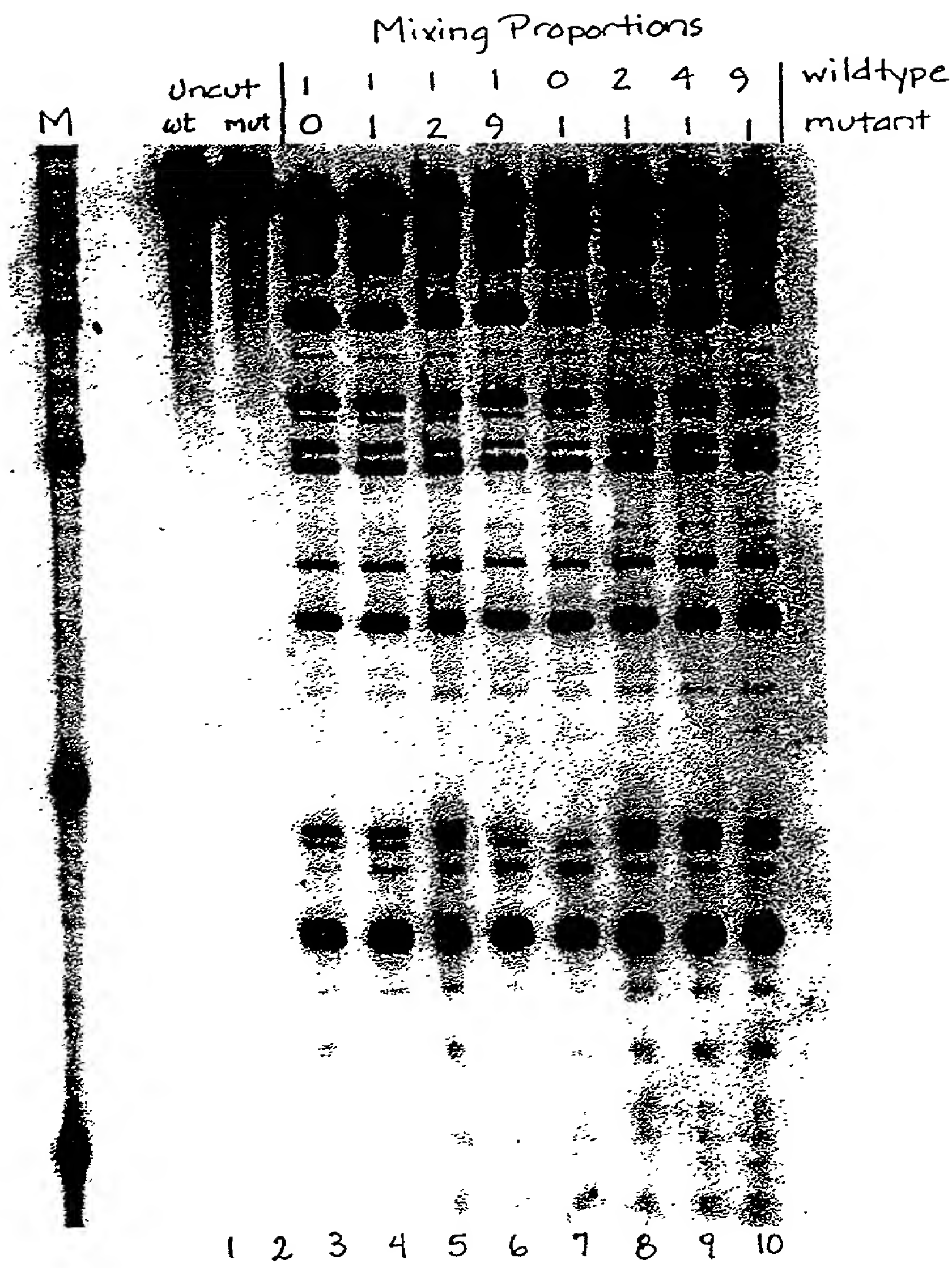


FIGURE 82

HCV1.1 (SEQ ID NO:121)
HCV2.1 (SEQ ID NO:122)
HCV3.1 (SEQ ID NO:123)
HCV4.2 (SEQ ID NO:124)
HCV6.1 (SEQ ID NO:125)
HCV7.1 (SEQ ID NO:126)

1 CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTGT 50
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT
CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT
CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAT GAGTGTCTGT
51 CAGCCTCCAG GACCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC 100
CAGCCTCCAG GACCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC
CAGCCTCCAG GTCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC
CAGCCTCCAG GACCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC
CAGCCTCCAG GCCCCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC
CAGCCTCCAG GACCCCCCCT CCGGGAGAG CCATAGTGGT CTGCGGAACC

HCV1.1
HCV2.1
HCV3.1
HCV4.2
HCV6.1
HCV7.1

101 GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-AAA 150
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-CAA
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC TTGGAT-CAA
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCTTTC GTGGATGTAA
GGTGAGTACA CCGGAATTGC CGGGAAGACT TTGGAT-AAA
GGTGAGTACA CCGGAATCGC TGGGTGACC TTGGAG-CAA

HCV1.1
HCV2.1
HCV3.1
HCV4.2
HCV6.1
HCV7.1

151 CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG 200
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG
CCCACTCTAT GCGGGGCGCAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG
CCCGCTCAAT ACCCAGAAAT TTGGGCGGTGC CCCCACAAGA TCACTAGCCG

HCV1.1
HCV2.1
HCV3.1
HCV4.2
HCV6.1
HCV7.1

201 AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCT 250
AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCTT
AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCTT
AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCTT
AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCTT
AGTAGTGTTG GGTCCGAAA GGCCCTTGTTG TACTGCCCTGA TAGGGTGCTT

HCV1.1
HCV2.1
HCV3.1
HCV4.2
HCV6.1
HCV7.1

251 GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC 282
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC
GCGAGTACCC CCGGAGGTCT CGTAGACCGT GC
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC

5

FIGURE 83

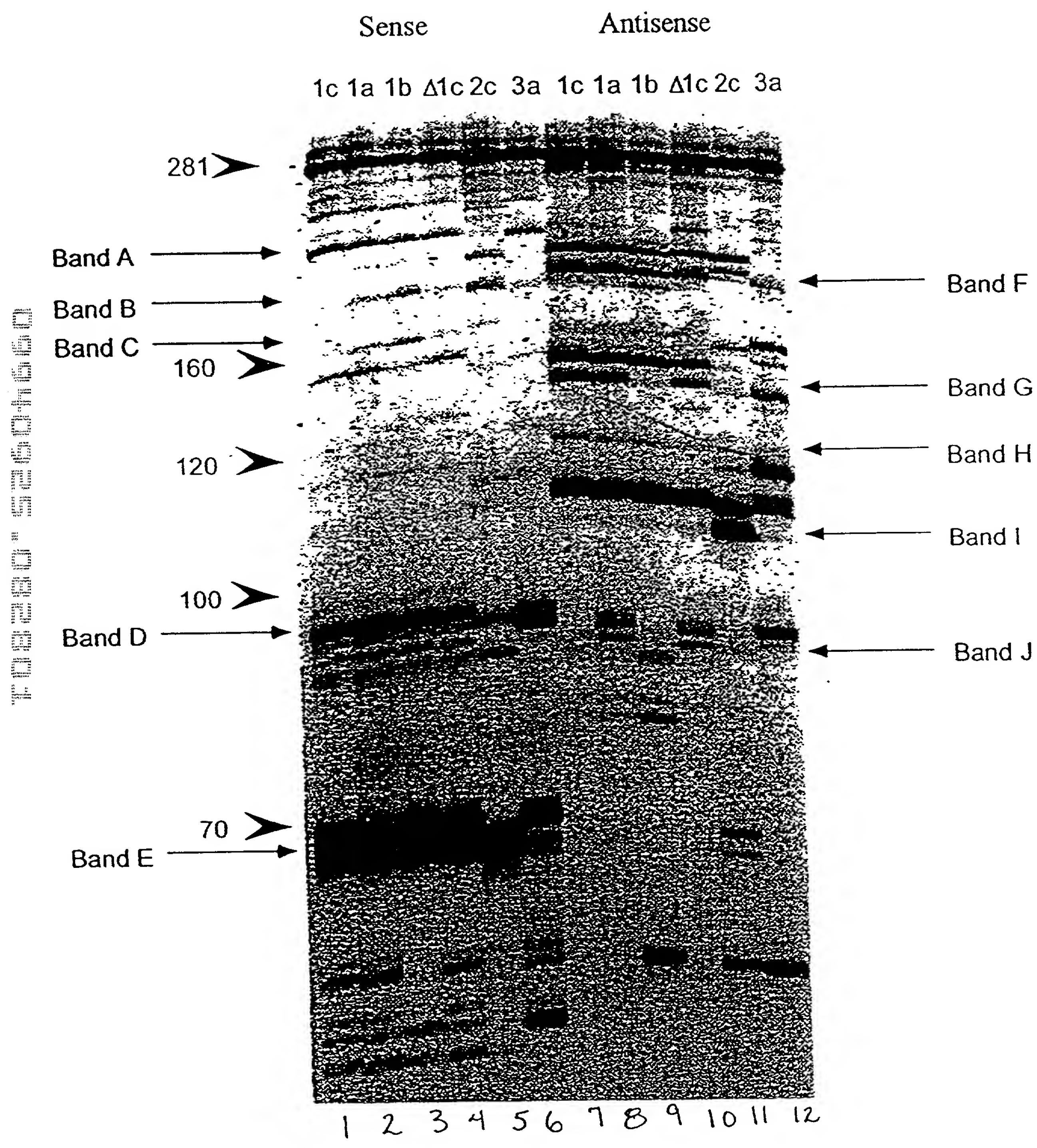


FIGURE 84

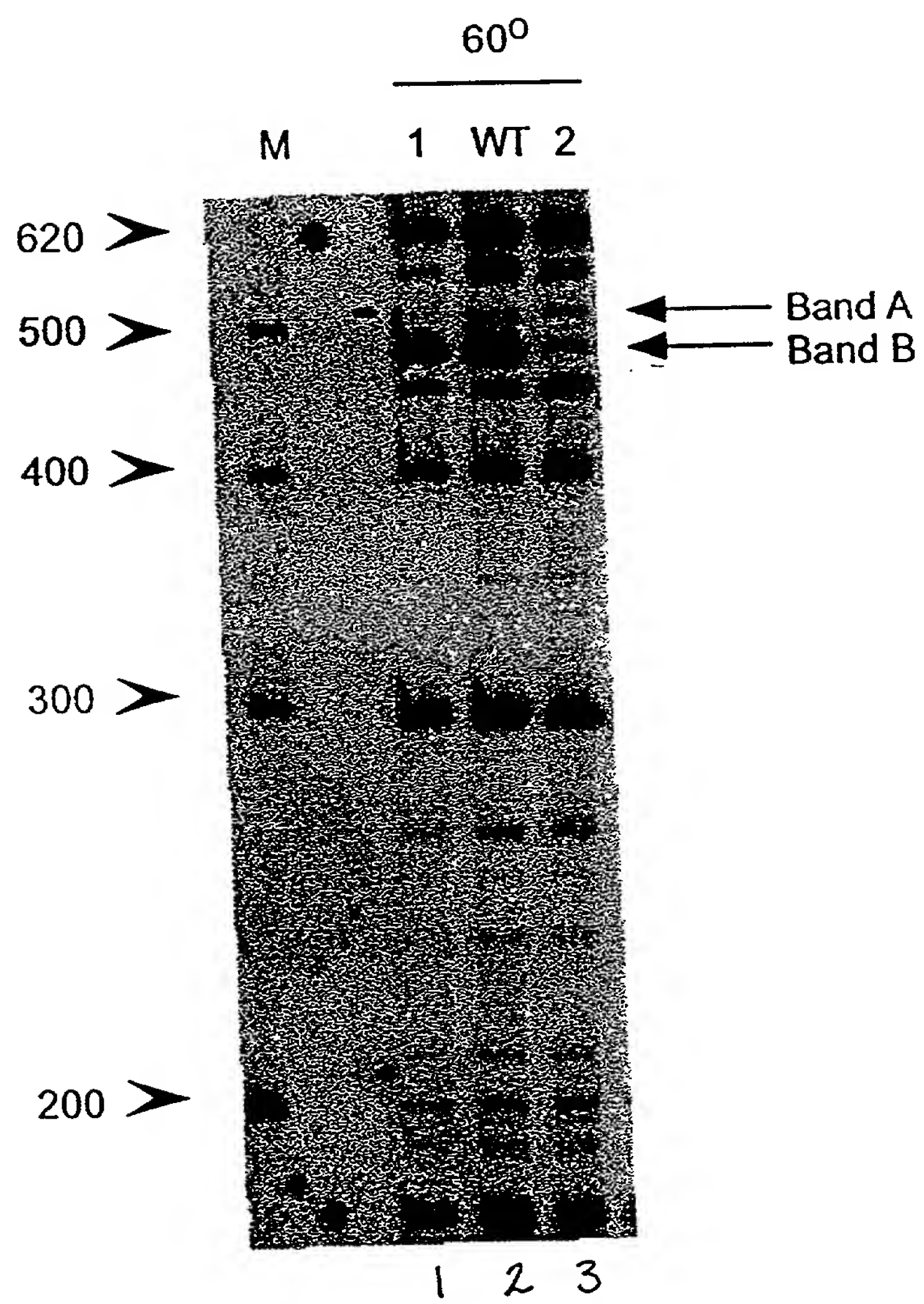
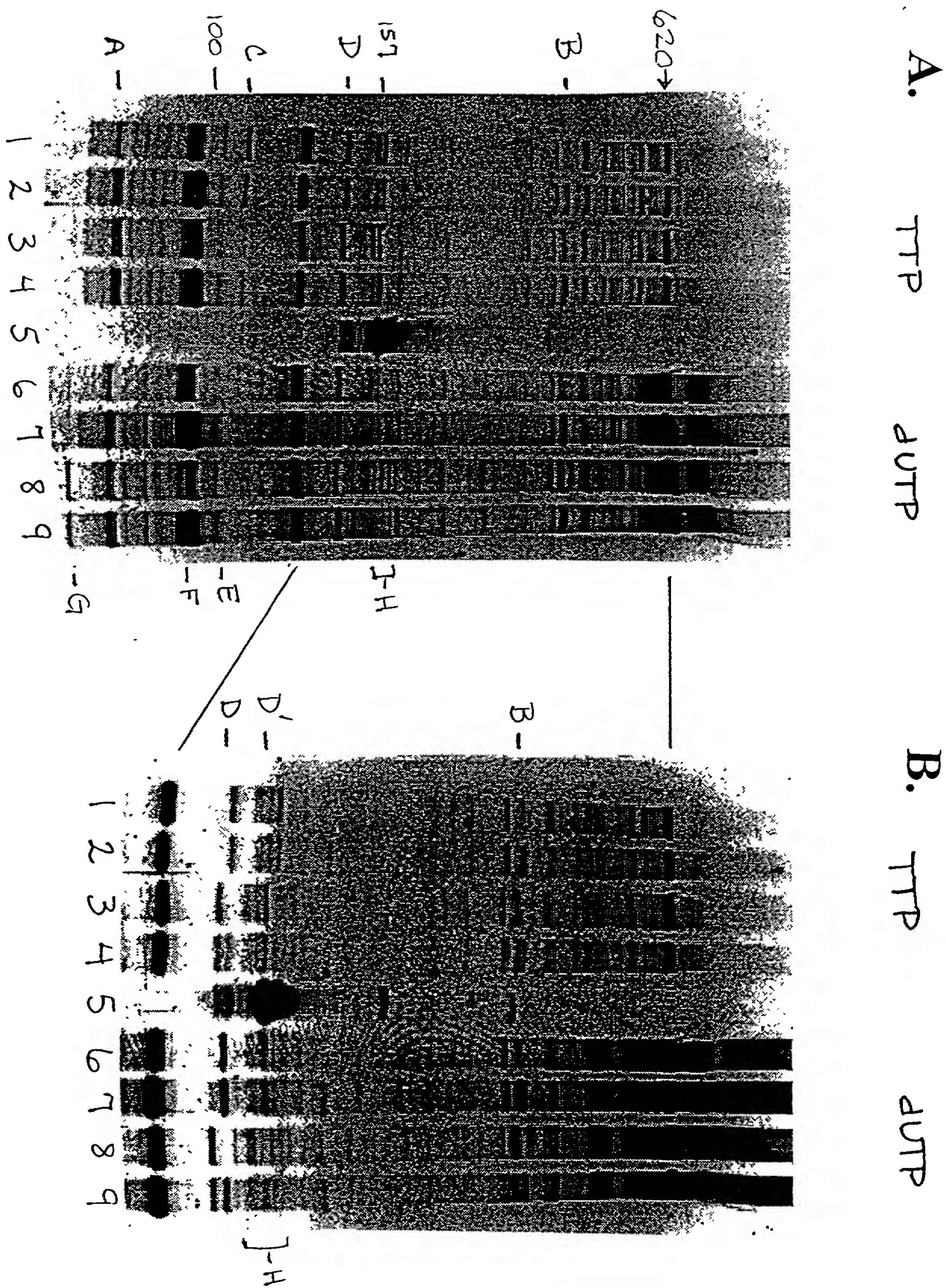


FIGURE 85



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FIGURE 86

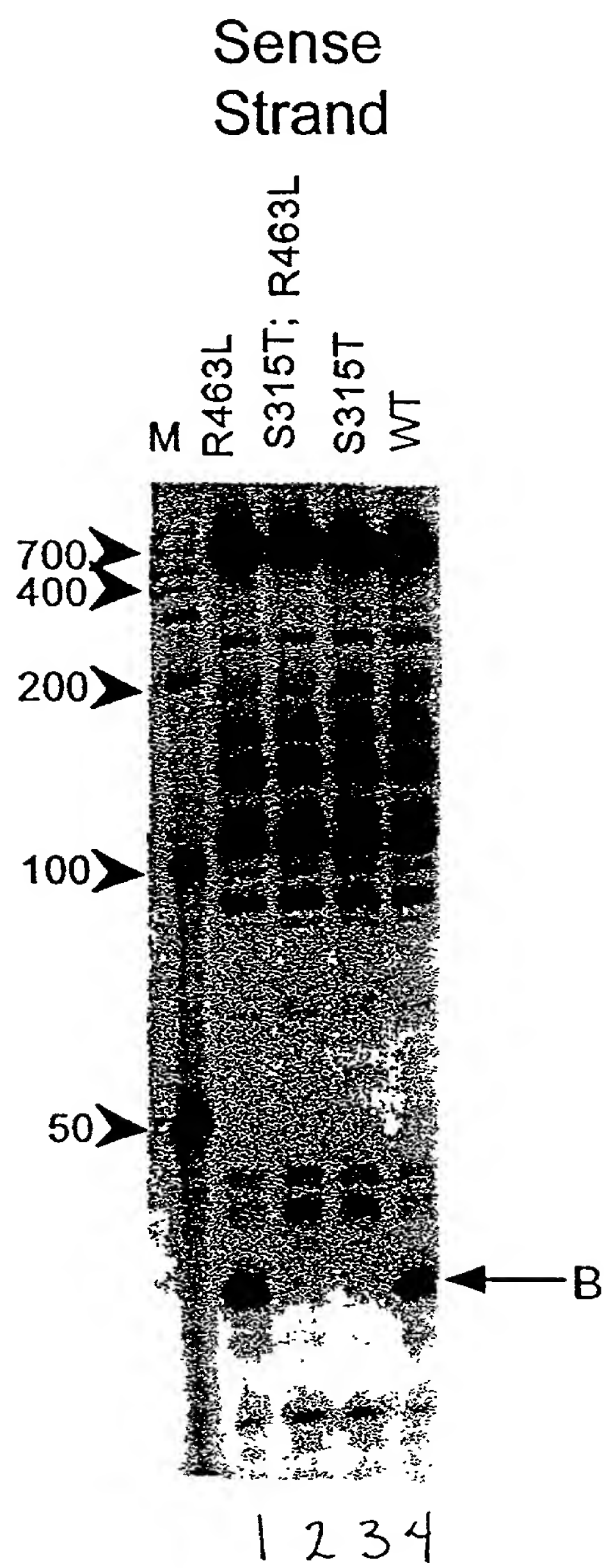


FIGURE 87

Antisense
Strand

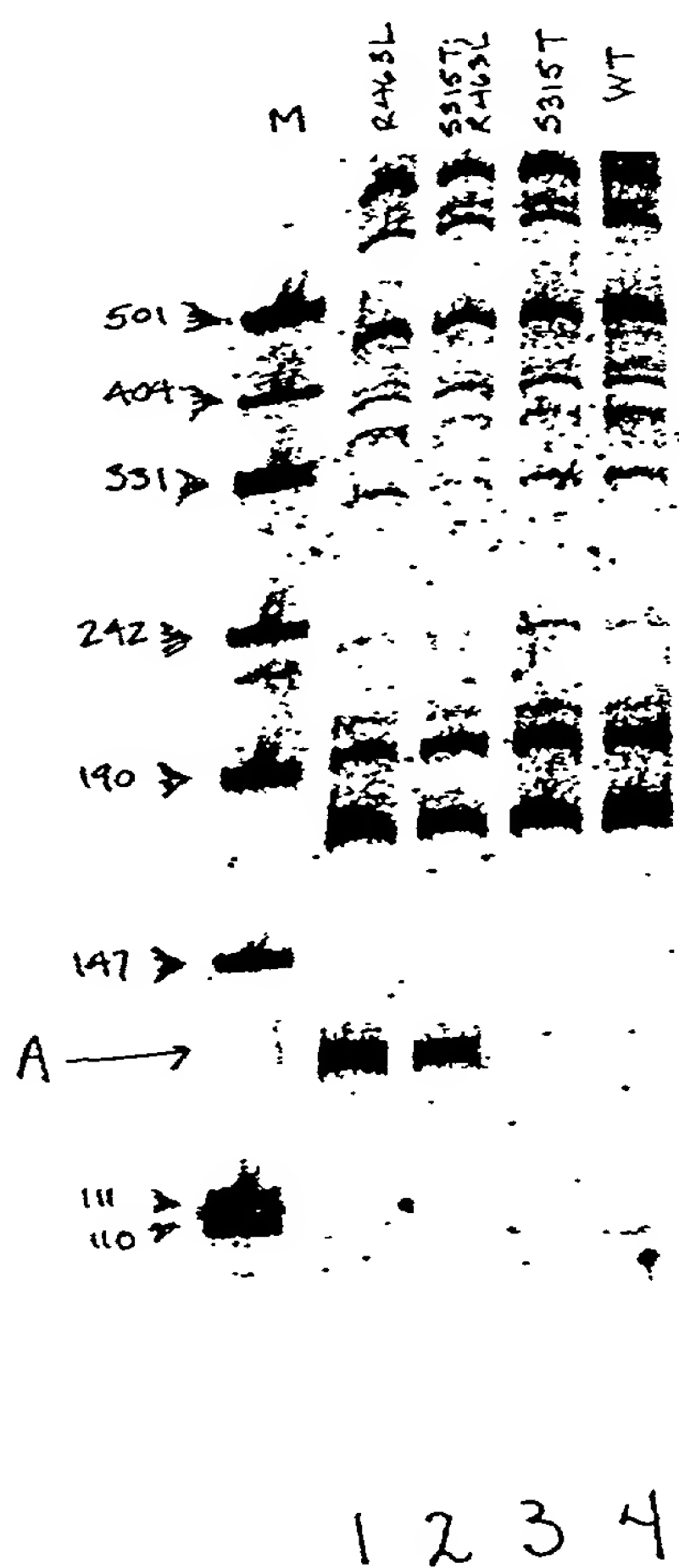


FIGURE 88

Sheet 1/2

10 20 30 40 50 60
AGA GTTTGATCCT GGCTCAG 1638
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA
TTTAACTTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

70 80 90 100 110 120
GGCGGAC GGGTGAGTAA ER10
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCATT

130 140 150 160 170 180
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA

190 200 210 220 230 240
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGGAGAAC GGTAGCCTAC ACGGGTCTAC

250 260 270 280 290 300
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT

310 320 330 340 350 360
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCACC
TGA GGATGCCCTC CGTCGTC 1659

370 380 390 400 410 420
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT
CCTTATAACG TGTTACCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCTTCCGGA

430 440 450 460 470 480
TCGGGTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT
AGCCCAACAT TTCATGAAAG TCGCCCCCTCC TTCCCTCATT TCAATTATGG AAACGAGTAA

490 500 510 520 530 540
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG
CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC

550 560 570 580 590 600
GGTGCAAGCG TTAATCGGAA TTACTGGGCG TAAAGCGCAC GCAGGCGGTT TGTAAAGTCA
CCACGTTCGC AATTAGCCTT AATGACCCGC ATTTGCGGTG CGTCCGCCAA ACAATTCAGT

610 620 630 640 650 660
GATGTGAAAT CCCC GGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC
CTACACTTTA GGGGCCCGAG TTGGACCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG

670 680 690 700 710 720
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC
CATCTCCCC CATCTTAAGG TCCACATCGC CACTTTACGC ATCTCTAGAC CTCCTTATGG

730 740 750 760 770 780
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTCCGAAAGC GTGGGGAGCA
CCACCGCTTC CGCGGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTTCG CACCCCTCGT

101

FIGURE 88

Sheet 4.2

790 800 810 820 830 840
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC
TTGTCCTAAT CTATGGGACC ATCAGGTGCG GCATTTGCTA CAGCTGAACC TCCAACACGG

850 860 870 880 890 900
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA
GAACTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAGCTGG CGGACCCCTC ATGCCGGCGT

910 920 930 940 950 960
AGGTAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT
TCCAATTTTG AGTTTACTTA ACTGCCCCCG GCGGTGTTCG CCACCTCGTA CACCAAATTA

970 980 990 1000 1010 1020
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTT CAGAGATGAG
AGCTACGTTG CGCTTCTTGG AATGGACCAG AACTGTAGGT GCCTTCAAAA GTCTCTACTC

1030 1040 1050 1060 1070 1080
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA
TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAACACT

1090 1100 1110 1120 1130 1140
GC AACGAGCGCA ACCC
AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC
TTACAACCCA ATTCAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCCG

1150 1160 1170 1180 1190 1200
ATG ACGTCAAGTC
ATG ACGTCAAGTC
CGGGAACCTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC
GCCCTTGAGT TTCCTCTGAC GGTCACTATT TGACCTCCTT CCACCCCTAC TGCAGTTCAG

1210 1220 1230 1240 1250 1260
ATCATGGCCC TTA
ATCATGGCCC TTACGA
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG
TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCGC

1270 1280 1290 1300 1310 1320
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TCGCTCGTAG TCCGGATTGG AGTCTGCAAC
TGGAGCGCTC TCGTTCGCCT GGAGTATTTC ACGCAGCATC AGGCCTAACC TCAGACGTTG

1330 1340 1350 1360 1370 1380
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT
AGCTGAGGTA CTTACGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC CACTTATGCA
GC CACTTATGCA

1390 1400 1410 1420 1430 1440
TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT
AGGGCCCCGGA ACATGTGTGG CGGGCAGTGT GGTACCCTCA CCAACGTTT TCTTCATCCA
AGGGCCCCGGA ACATG

1450 1460 1470 1480 1490 1500
AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGAAGTGGGT GAAGTCGTAA
TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTACGCATT

1510 1520 1530 1540 1550
CAAGGTAACC GTAGGGGAAC CTGCGGTGTTG ATCACCTCCT TA.....
GTTCCATTGG CATCCCCTTG GACGCCAACC TAGTGGAGGA AT.....

SB-1

SB-3
SB-4SB-3
SB-4

1743

1743

102

1638 (SEQ ID NO:151)
E.colirrsE (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGAGGCTTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCTGCTTAATACATGCA
stp.aureus (SEQ ID NO:160) 0 ..TTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCTTAATACATGCA
AGAGTTTGATCCTGGCTCAG

ER10 (SEQ ID NO:152)
E.colirrsE
Cam.jejun5
stp.aureus
60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT----GAAGCTTCTAGCTTGCTAGAGTGGA----TTAGTGGCGCACGGG
61 AGTCGAGCGAA----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGCGGACGGG
GGCGGACGGG

ER10
E.colirrsE
Cam.jejun5
stp.aureus
TGAGTAA
114 TGAGTAAATGTCTGGGA-AACTGCCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATA
114 TGAGTAAAGGTATAGTTAATCTGCCCTACACAGAGGACACAGTTGGAAACGACTGCTAATA
113 TGAGTAAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA
175 CCGCATAAC----GTGCAAGAC----CAAGAGGGGACCTTCG-GGCCTCTTG
176 CTCATACCTCCTGCTTAACACAGTTAGTAGG-GAAAG----TTTTT----CG
175 CCGGATAAATATTTGAACCGCATGGTTCAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirrsE
Cam.jejun5
stp.aureus
221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGGTAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirrsE
Cam.jejun5
stp.aureus
1659 (COMPL)
283 TCCCTAGCTGGTCTGAGAGGATGACCCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
ACTCCTA

E.colirrsE
Cam.jejun5
stp.aureus
1659 (COMPL)
345 CGGGAGGCAGCAGTGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCCGTG
345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAAACCCCTGACGCGCAACGCCCGTG
353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCCGTG
CGGGAGGCAGCAG

E.colirrsE
Cam.jejun5
stp.aureus
407 TATGAAGAAGCCCTTCGGGTTGTAAAGTACTTTCAGCGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGAGCGGTAAACTCCTTTTCTTAGGGAAG----AAAT
415 AGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAATATGTGTAAGTAAC

E.colirrsE
Cam.jejun5
stp.aureus
468 ACCTTTGTCTATTGACGTTACCCCGCAGAAAGACCCGGCTAACTCCGTGCCAGCAGCCGCG
455 C---------TGACGGTACCTAAGGAATAAGCACCCGGCTAACTCCGTGCCAGCAGCCGCG
476 -TGTCACATCTTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

E.coli	530	GTAATACGAGGGTGC
Cam.jejun	506	GTAATACGAGGGTGC
Stp.aureus	538	GTAATACGAGGGTGC
E.coli	592	GTTAAGTCAGATGTG
Cam.jejun	568	ATCAAAGTCTCTTGT
Stp.aureus	600	TTTAAAGTCTGATGT
E.coli	654	GAGTCTCGTAGAGGG
Cam.jejun	630	GAGTGAGGAGAGGCA
Stp.aureus	662	GAGTGCAGAAAGAGG
E.coli	716	ATACCGGTGGCGAAG
Cam.jejun	692	ATACCCATTGCGAAG
Stp.aureus	724	ACACCAGTGGCGAAG
E.coli	778	GCAAACAGGATTAGAT
Cam.jejun	754	GCAAACAGGATTAGAT
Stp.aureus	786	TCAAACAGGATTAGAT
E.coli	840	C-CTTGA-GGCGTGGCT
Cam.jejun	816	G-CTAGT-CATCTCAGT
Stp.aureus	848	GT-TTCCGCCCTTAGT
E.coli	900	AAGGTTAAAACTCAA
Cam.jejun	876	AAGATTAAAACTCAA
Stp.aureus	909	AAGTTGAAACTCAA
E.coli	962	CGATGCAACGCGAAG
Cam.jejun	938	CGAAGATACGCGAAG
Stp.aureus	971	CGAAGCAACGCGAAG
E.coli	1024	GTG--CCTTCGGG--AA-
Cam.jejun	1000	GTGCTAGCTTGCTAGAA-
Stp.aureus	1033	TTCC-CCTTCGGG--GG
SB-1		GCAACGAGCGCAACCC
E.coli	1081	AATGTTGGGTTAAGTCC
Cam.jejun	1061	GATGTTGGGTTAAGTCC
Stp.aureus	1092	GATGTTGGGTTAAGTCC

FIGURE 89

Sheet 3/3

SB-3 (SEQ ID NO:157) ATGACGTCAAGTCATC
 SB-4 (SEQ ID NO:154) ATGACGTCAAGTCATC
 E.colirrhE 1142 GGGAACCTCAAGAGAGACTGCCAGTGATAACTGGAGGAAGGTGGGATGACGTCAAGTCATC
 Cam.jejun5 1122 GAGCACTCTAAATAGACTGCCCTTCG-TAAGAGAGAGGAAGGTGTGGACGACGTCAAGTCATC
 Stp.aureus 1152 GGGCACTCTAAGTTGACTGCCGGGTGACCAACCAGAGGAAGGTGGGATGACGTCAATCATC

SB-3 ATGGCCCTTA
 SB-4 ATGGCCCTTACGA
 E.colirrhE 1204 ATGGCCCTTACGACCAAGGCTACACACGTGCTACAAATGGCCGATACAAAGAGAGAGGACCTC
 Cam.jejun5 1183 ATGGCCCTTATGCCCCAGGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC
 Stp.aureus 1214 ATGCCCCCTTATGATTTGGGCTACACACGTGCTACAAATGGACAATACAAAGGCGAGCAACC

E.colirrhE 1266 GCGAGAGCAAGCGGACCTCATAAAGTGCCTGCTAGTCCCGGATTGGAGTCTGCAACTCGACTC
 Cam.jejun5 1245 GCGAGGTGGAG-CAAATCTATAAATATGTCCAGTTGGGATTGTCTCTGCAACTCGAGAG
 Stp.aureus 1276 GCGAGGTCAAGCAAAATCCCATAAAGTTGTCTCAGTTGGGATTGTAGTCTGCAACTCGACTA

E.colirrhE 1328 CATGAAGTCGGAATCGCTAGTAATCGTGATCAGA-ATGCCACGGGTGAATACGTTCCCGGGC
 Cam.jejun5 1306 CATGAAGCCGGAAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
 Stp.aureus 1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
 1743 (compl) CCGTGAATACGTTCCCGGGC

E.colirrhE 1389 CTGTACACACCGCCCCGTCACACCATGGAGTGGGTTGCAAAAGAAAGTAAGTTAGCTTAACCT
 Cam.jejun5 1368 CTGTACTCACCGCCCCGTCACACCATGGAGTTGATTCTCACTCGAAGCCCGAATACT--A-A
 Stp.aureus 1399 ATTGTACACACCGCCCCGTCACACCATGAGAGTTTGTAAACACCCGAAGCCCGTGGAGTAACCT
 1743 (compl) CTGTAC

E.colirrhE 1451 TCG-GGAGGGCGCTTACCACTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCG
 Cam.jejun5 1427 AC--T-AGTTACCGTCCACAGTGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
 Stp.aureus 1461 TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAACCG

E.colirrhE 1512 TAGGGGAACCTGCGGTTGGATCAACCTCCTTA---
 Cam.jejun5 1485 TAGGAGAACTGCGGTTGGATCAACCTCCT---
 Stp.aureus 1523 TATCGGAAGGTGCGGCTGGATCAACCTCCTTCT-

094099 094099

105

FIGURE 90

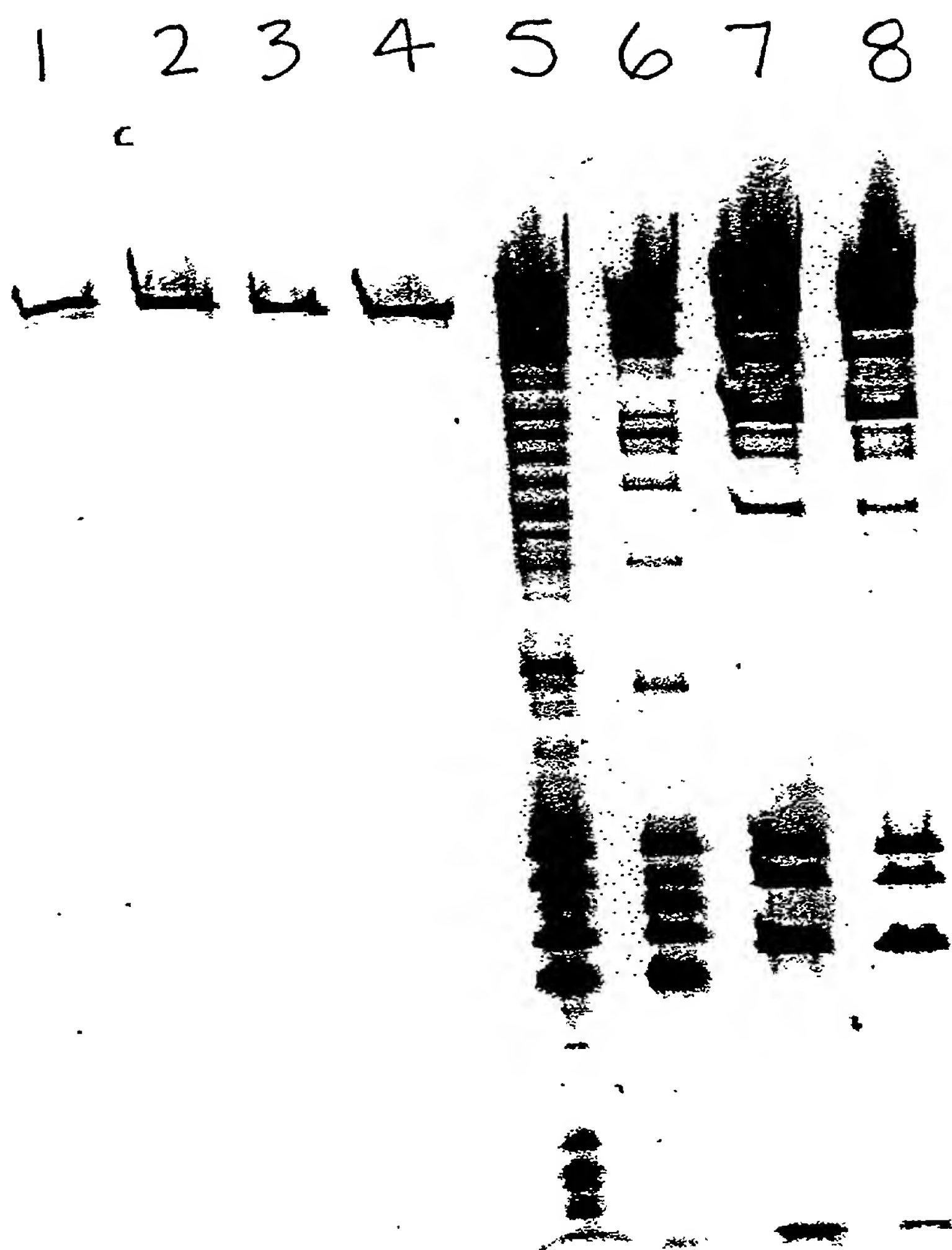
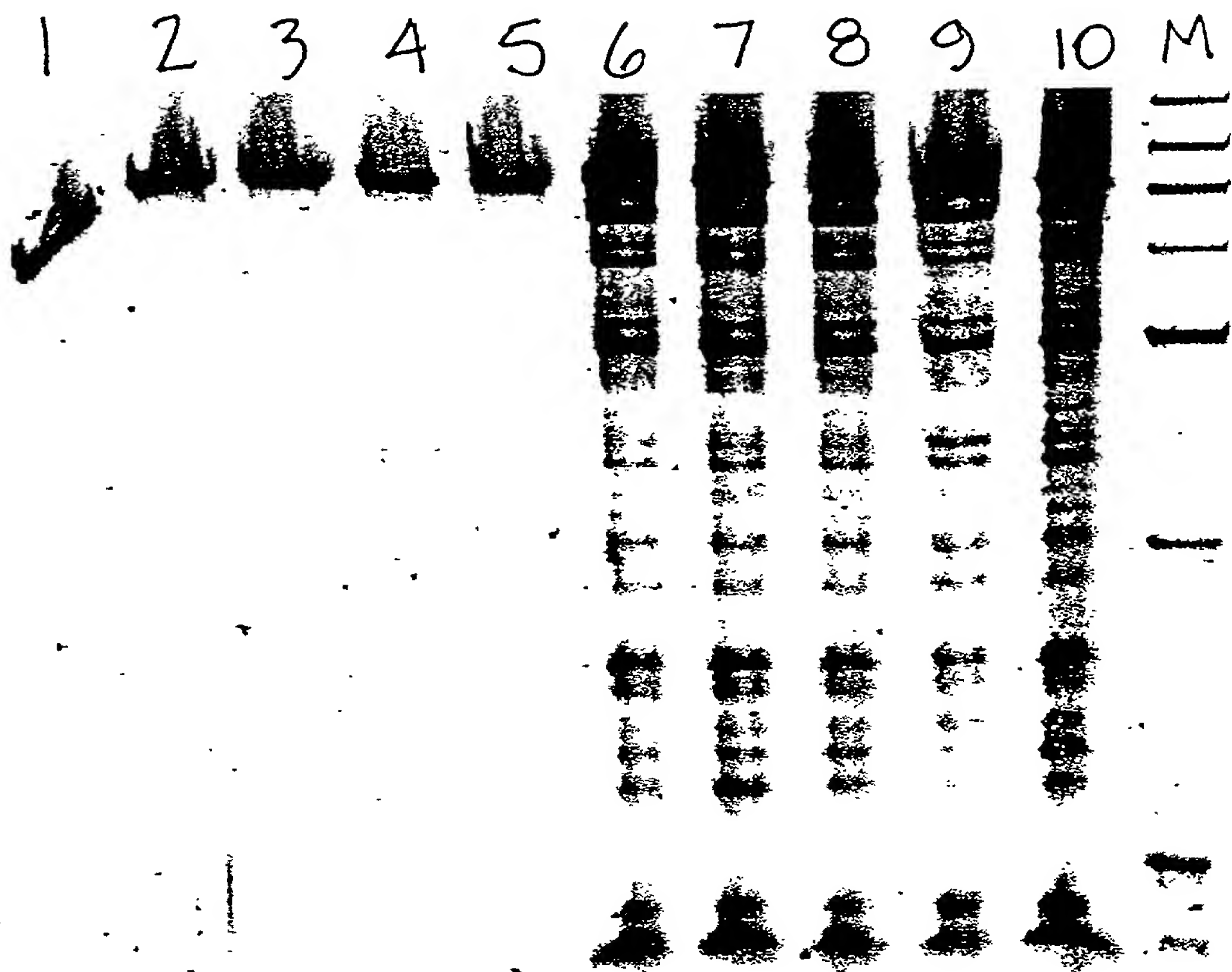


FIGURE 91

A.



B.

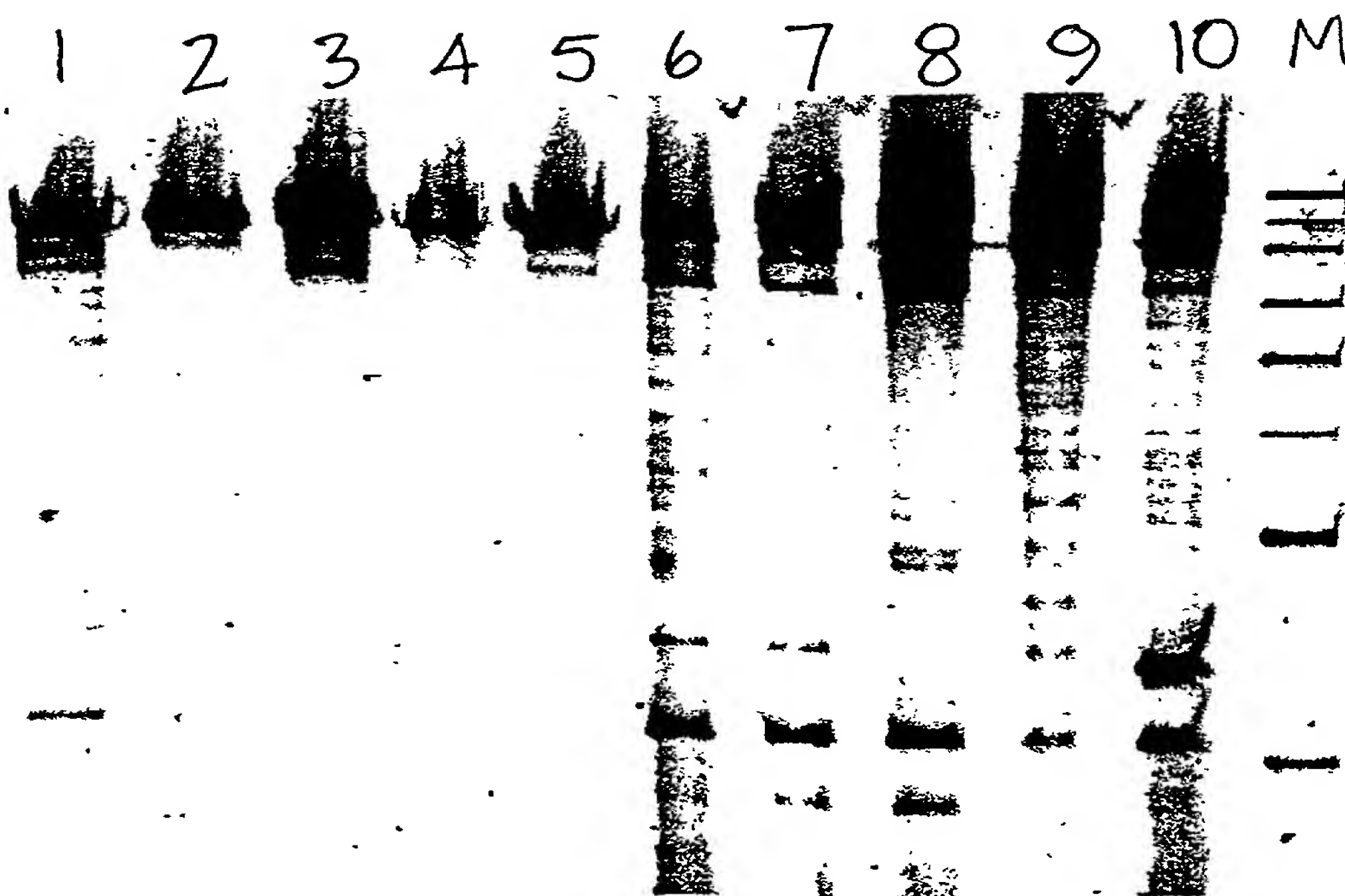


FIGURE 92

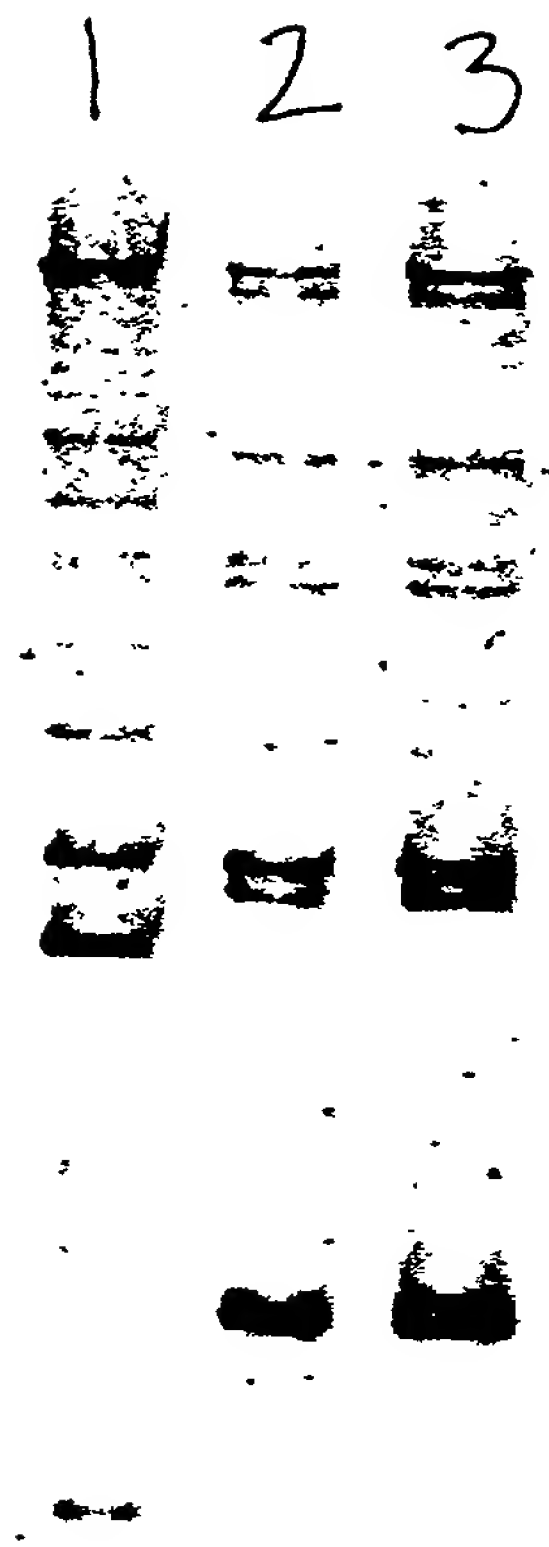
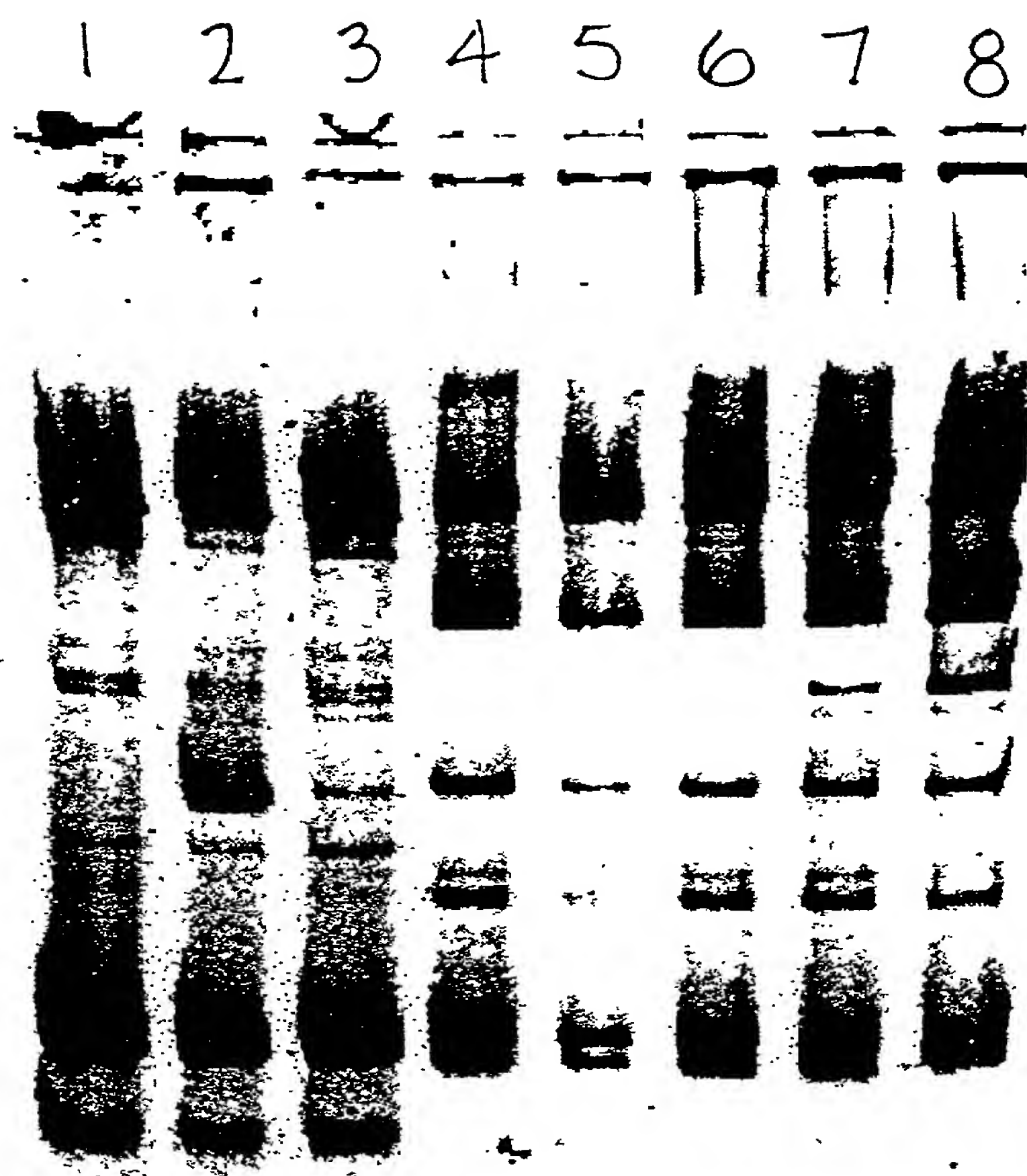


FIGURE 93



094030 094030

FIGURE 94

